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2735 bp mRNA linear PLN 14-JUL-2003 Solamum tuberosum BEL1-related homeotic protein S (Be15) mRNA, AP406697
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Chen, H., Rosin, F.M. and Hannapel, D.J.
A KNOX protein of potato interacts with several members of the TALE family of transcription factors
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1 (bases 1 to 2735)
Chen,H., Rosin,F.M., Prat,S. and Hannapel,D.J.
Interacting transcription factors from the three-amino acid loop extension superclass regulate tuber formation
Plant Physiol. 132 (3), 1391-1404 (2003)
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Chen, H., Rosin, F.M. and Hannapel, D.J.
Direct Submission
Submitted (07-A0722001) Department of Horticulture, Iowa State
University, 257 Horticulture Hall, Ames, IA 50011-1100, USA
Location/Qualifiers
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/product="BEL1-related homeotic protein 5"
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/organism="Solanum tuberosum"
/mol type="mRNA"
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                      GCTGCACAAGAGCTTCTTGATGAAGTTGTTAATATTTGTTGGAAAAAGCATCAAAGGAGAT
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WRPQRGLPERAVSVLRAMLFEHLPVPVBCSDKIMLAKQTGLTRSQVSNWFINBLYDQ
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/clone="132117F"
/hissue_type="fxuit"
/hote="TXBC46"
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larity 91.1%; Pred. No. 0;
Conservative 0; Mismatches
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PLN 11-MAY-2004

2687 bp mRNA linear Pl Lycopersicon esculentum clone 132117F, mRNA sequence. BT013459.1 GI:47104874
FLI_CDNA.

RESULT 2 BT013459 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOUNCE ORGANISM

Lycopersicon esculentum (tomato)
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 2687)

REFERENCE

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YTTTDTQQHLQQQQNQHQLLFLNSAPAGGNALSHANIQHAPLQQQHFVGYPLPAVSLH
DQINHHGLLQRWMNONQDQSQQYI YESTYNAYTIRGTTDLAGQLAFQREIYUVBTTP
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SSLLQDGTTQAR I STSTI STSTTAGASLHHAHNFSFLGSFNMRNTTTTVDHI ENNAKK
PRNHDMHKFSPSSILSSVBMEARARESTNKGFTNPLMAAYAMGDFGRFDPHDQQMTAN
FHGRNNGVSLTLALPPBENALAMPVSQQNYLSNELGSRPBI GSHYNRMGYENI DFQSGNK
RFFTQLL PDFVTGLLGT"
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Pred. No. 0;
Mismatches 132; Indels
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100. .2199
/gene="BL2"
/note="TBL2"
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Best Local Similarity 90.9%;
Matches 2418; Conservative
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SOURCE Solanum tuberosum (potato) ORGANISM Solanum tuberosum (potato) I (bases 1 to 189) AUTHORS (hen. H., Rosin.F. M., 2011 1391-1404 (2003) Interacting transcription factors from the three-amino acid loop (potato) Interacting transcription factors from the three-amino acid loop (potato) Interacting transcription factors (potato) AVENDER (2 (bases 1 to 189) AUTHORS (hen.H., Rosin.F. M. and Hannapel, D.J. AVENDER (2 (bases 1 to 189) AUTHORS (hen.H., Rosin.F. M. and Hannapel, D.J. TITLE (amily of transcription factors JONENAL (potato) AUTHORS (hen.H., Rosin.F. M. and Hannapel, D.J. TITLE (potato) AUTHORS (hen.H., Rosin.F. M. and Hannapel, D.J. TITLE (potato) AUTHORS (hen.H., Rosin.F. M. and Hannapel, D.J. TITLE (house 1 to 189) AUTHORS (hen.H., Rosin.F. M. and Hannapel, D.J. TITLE (hen.H., Rosin.F. M. and Hannapel, D.J. TITLE (hen.H., Rosin.F. M. and Hannapel, D.J. TITLE (house 1 to 189) AUTHORS (hen.H., Rosin.F. M. and Hannapel, D.J. TITLE (house) AUTHORS (hen.H., Rosin.F. M. and Hannapel, D.J. TITLE (house) AUTHORS (hen.H., Rosin.F. M. and Hannapel, D.J. TITLE (house) AUTHORS (hen.H., Rosin.F. M. and Hannapel, D.J. TITLE (house) AUTHORS (house) AUTHOR	Query Match 19.2%; Score 524.6; DB 8; Length 1898; Best Local Similarity 71.3%; Pred. No. 7.5e-96; Matches 813; Conservative 0; Mismatches 274; Indels 54; Gaps 7;	Oy 729 AACATTAGATGGAAGTTCTAGCAACATGGTTTTAGGCTCTAAGTATCTGAAAGCTGCACA 788	Oy 789 AGAGCTTCTTGATGAAGTTGTTAATATTGTTGGAAAAAGCATCAAAGGAGATGATCAAAA 848 	OY 849 GAAGGATAATTCAATGAATAAGAATCAATGCCTTTGGCTAGTGATGTCAACAACTAATAG 908	Oy 909 TTCTGGTGGTGGTGGAGGGGGGGAGAAATGAAGTTGCTGTTGAGCTTACAAC 968
1744 TCCTTCCTTGGTTCATTCAACATGGATAATACTACTACTTGTTGATCATTGAAAAC	CTTCTAGTTCCTTGAGAAGATTGATACAACT 	2516 TTTTCTTTGGGTTGGCTTGGAGTACTATTTTAAGTTATTGG 2558	2559 AAACTAGCTATAGTAAATGTTGTAAAGTTGTGATATTGTTCCTCCTCAATTTGCATATA 2616 	2617 ATTTGAAATATTTGTACCTA 2637 	4 8 AF406698 1898 bp mRNA linear PLN 14-JUL-2003 ION Solanum tuberosum BEL1-related homeotic protein 11 (Bel11) mRNA, partial cds. ON AF406698 AF406698.1 GI:22652116 S .

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1 (bases 1 to 2128)
Chen, H., Rosin, F.M., Prat, S. and Hannapel, D.J.
Interacting transcription factors from the three-amino acid loop
extension superclass regulate tuber formation
Plant Physiol. 132 (3), 1391-1404 (2003)
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Chen, H., Rosin, F.M. and Hannapel, D.J.
Direct Submission
Submitted (07-AUG-2001) Department of Horticulture, Iowa Statuly 257 Horticulture Hall, Ames, IA 50011-1100, USA
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                                                                                                                           Chen, H., Rosin, F.M. and Hannapel, D.J.
A KNOX protein of potato interacts with several
family of transcription factors
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/organism="Solanum tuberosum"
/mol type="mRNA"
/cultivar="Desiree"
/db_xref="taxon:4113"
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/note="StBel29"
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicacea; Arabidopsis.

(bases 1 to 2043)

Cheuk, R., Chen, H., Kim, C.J., Shinn, P., Bowser, L., Carninci, P., Dale, J. M., Hayashizaki, Y., Hsuan, V.W., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Southwick, A., Toriumi, M., Wong, C., Wu, H.C., Yamada, M., Yu, G., Yuan, S., Shinozaki, K., Davis, R.W., Arabidopsis ORF clones
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Cheuk, R., Chen, H., Kim, C.J., Shinn, P., Bowser, L., Carninci, P.,
Dale, J.M., Hayashizaki, Y., Hsuan, V.W., Ishida, J., Jones, T.,
Ramiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lih, J., Miranda, M.,
Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L.,
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                                                               749 cagaagcagccoggaaacgrccgcrccacragcacacacacagagagagaaracaga
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                                                                   CTAAAGGATGCAATTGCTGAGCAAGTAAAGGCGACGAGGAATTTAGGTGAAGAGAA 1221
                                                                                                                                                   GGCTTGGGAGGGAAAATCGAAGGCTCAAGACTCAAATTTGTGGACCATCATCTAAGGCAA 1281
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kukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                               127 TTGCCCGAACGAGCTGTTTCTGTTCTTCGCGCTTGGCTTTTTGAACATTTCTCCCCCATCCT
607 AGTTTGGGAGGGAAGATTGAAGGTTCAAGGCTTAAATTTGTTGATAATCAGCTAAGACAG
                                                                                                                                                                                                                                                                                                                                                                                                       TACCCAAAGGATTCAGACAAAATCATGCTTGCTAAGCAAACGGGGCTAACAAGGAGCCAG
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                                                                                         CAACGCGCGCTGCAACAGATAGGAATGATGCAACCAAATGCTTGGAGACCCCAAAGAGGT
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Stress-regulated genes of plants, transgenic plants containing same, and methods of use
Patent: WO 0216655-A 1337 28-FEB-2002;
The Scripps Research Institute (US); Syngenta Participations Patents
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| Occaniam="Arabidopsis thaliana"
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|db_xref="taxon:3702"
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       ACCAGCAGATGCAGATGGTGTCTTTCGTTCGAGCAAGCGGCAGGGATAGGATAGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1337 GAGGTTTACCTGAAAGAGCTGTCTCTTCGTGCTTGGCTTTTCGAGCATTTTCTTC
                                                                             TGAAGAAAGCAAAACTTAGTAACATGCTTCATGAGGTGGAGCAGAGATATAGACAGTACC
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                                                                                                                                              ATCACCAAATGCAAATAATTGTATTATCATTTGAGCAAGTAGCAGGAATTGGATCAGCCA
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PERAVSVLRAMLFEHFLHPPYPROSDKHMLAKQTGLTRSQVSNRFINARNHNGDLEG
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VTGMQGSPKRLFTDETNMQPINADFSSNRETAWTLLEERQGIRSDGGYPFMGHFQPY

RRVKIGETEEYGPATINGGSSTTTAMSSAAAAAYNGWNIQNQKRYVAQLLPDFVA"
Sakurai,T., Satou,M., Seki,M., Southwick,A., Toriumi,M., Wong,C., Wu,H.C., Yamada,K., Yu,G., Yuan,S., Shinozaki,K., Davis,R.W.,
Direct Submission

Submitted (15-WAY-2003) Salk Institute Genomic Analysis Laboratory (SIGnAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                                                                                                                                                                                                                                                                                                                         The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL cDNAs: Cheuk, R., Chen, H., Kim, C., J., Shinn, P., Bowser, L., Chan, M.M., Chang, C.M., Bale, J.M., Hsuan, V.W., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Miranda, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S., Davis, R.W., Theologis, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S
                                                                                                                                                                                    RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN trabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cheuk, R. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs. Location/Qualifiers
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/note="This clone is in pUNI 51"
1. .2043
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/db_xref="taxon:3702"
/chromosome="2"
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Arabidopsis thaliana BEL1-like homeodomain 1 (BLH1) mRNA, complete
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Arabidopsis thaliana

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 2385)

Pidkowich, M.S., Samach, A., Modrusan, Z. and Haughn, G.W.

A family of BELI-like homeodomain (BLH) proteins in Arabidopsis thaliana
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Pidkowich, M.S., Samach, A., Modrusan, Z. and Haughn, G.W.
Direct Submission
Submitted (26-FEB-2001) Botany, University of British Columbia, #3529 - 6270 University Blvd., Vancouver, BC V6T 1Z4, Canada Location/Qualifiers
                                                                                                                                              1109 gagcircirchachachgangantahchachtcentcenarahargcirgaadcreaac
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378 TGCCTTTGGCTAGTGATGTCAACACTAATAGTTCTGGTGGTGGTGAAAGTAGCAGCAGGC
                                                     689 ATGATAAACCTGTCGGAGAATCATCGGCCGGCGCTGGAGGAGAAGGTTCCGGTGGCGGAG
                                                                                                              938 AGAAAAATG-----AAGTTGCTGTTGAGCTTACAACTGCTCAAAGACAAGAACTTCAAA
                                                                                                                                                                                                                            1052 ATCACCAAATGCAAATAATTGTATTATCATTTGAGCAAGTAGCAGGAATTGGATCAGCA
                                                                                                                                                                                                                                                                                                                                                                                       869 ACCAGCAGATGCAGATGCTGTTCTTCGTTCGAGCAAGCGGCAGGGATAGGATCAGCGA
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/ devidence=experimental
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/ product="putative homeodomain transcription factor"
/ product="putative homeodomain transcription factor"
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/ MALHEYPEQXYRQYHQQMQNTSSFEQAAGIGSAKSYTSLALKTISTGPRCLKGAIAGQ
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/ QMDBXRFDVVSDQELMAQRYSGNNNGVSLTGLPHCDSLSSTHHQGFWQY
/ GMDSRXRFDVVSDQELMAQRYSGNNNGVSLTGLPHCDSLSSTHHQGFWQY
/ GHOE="A4.2935940"
                 Sakurai,T., Satou,M., Saki,M., Shinn,P., Southwick,A., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.
Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.
Direct Submission
Submitted (16-APR-2012)
Submitted (16-APR-2012)
Flant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
The RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAs (RAFL cDNA : RIKEN
Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J.,
Satou,M., Sakurai,T., Carninci,P., Kawai, J.,
Hayashizaki,Y. and Shinozaki,K.
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Narusaka, M., Nguyen, M., Palm, C.J.,
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                                                                                                                                                                                                                                                                                                                                    The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the PUNI (ORF) clones using the RAFL CDNAs: Yamada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Chrumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Chen, H., Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Lam, B., Lin, J., Mayers, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.
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/mol_type="mRNA"
/db_xref="taxon:3702"
/chromosome="2"
Meyers, M.C., Miranda, M.,
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/note="This clone is
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this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC) contributed equally to this work as PIs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="homeodomain protein BLH1; transcription factor; capable of heterodimerization with KNAT proteins; similar to predicted homeodomain protein presented in GenBank Accession Number AAD21463"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITIAGGCICTAAGTATCTGAAAGCTGCACAAGAGCTTCTTGATGAAGTTGTTAATATTG 817
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Pred. No. 2.5e-55;
0; Mismatches 264; Indels
                                                                                                                                                                                                                       product="BEL1-like homeodomain 1"
               thaliana
             organism="Arabidopsis
                            /mol_type="mRNA"
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/chromosome="II"
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Arabidopsis thaliana

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatorphyta, Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases 1 to 2572)

Sa Samada, K., Liu, S.X.; Sakano, H., Dham, P. K., Banh, J., Chung, M.K.,

Goldsmith, A.D., Lee, J. M., Quach, H.L., Toriumi, M., Yu, G., Bowser, L.,

Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Kan,

Jones T., Kaniya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B.,

Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T.,

Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K.,

Arabidopsis Full Length cDNA Clones

Unpublished

S (bases 1 to 2572)

Yamada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M.,

Davis, R. W., Goldsmith, A.D., Lee, J. M., Onodera, C.S., Quach, H.L.,

Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Lam, B.,

Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B.,

Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J.,

Shinozaki, K., Davis, W., Bcker, J.R. and Theologis, A.

Birect Submission
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thaliana putative homeodomain transcription factor
mRNA, complete cds.
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RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN
Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J.,
Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                         1457 GCCAGGTGTCTAACTGGTTCATAAATGCTCGAGTTCGATTATGGAAGCCAATGGTAGAAG
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AY099854 2002 2578 bp mRNA linear PLN 06-MAY-2002 Arabidopsis thaliana putative homeodomain transcription factor (At2935940) mRNA, complete cds.
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Southwick,A., Karlin-Neumann,G., Lam,B., Miranda,M., Palm,C.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (24-APR-2002) DNA Sequencing and Technology Center,
niversity, 855 California Avenue, Palo Alto, CA 94304,
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                                                                                                                                         AATCATACACTCAATTAGCTTTGCATGCAATTTCGAAGCAATTCAGATGCCTAAAGGATG
                                                                                                                                                                                            AGTCATACACGTCGCTAGCATTGAAAACCATATCAAGACAGTTCCGTTGCTTGAAAGAGG
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Submitted (24-APR-2002) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 9430
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Hayashizaki,Y. and Shinozaki,K.
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QLFSSKKGSCCNDKPVGESSAAGAGGSCGGARAAGKRPVELGTABROEIDDRNAKS
QLFSSKKGSCCNDKPVGESSAAGAGGSAKSYTSLALKTI SROFRCLKEAIAGO
IKAANKSLGEEDSVSCOWRFEGSRLKRVDHLROQRALOQLGANI OFFSNNARFPORGL
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VTGMGGSPKRLRTSDETWMOPINADFSSNBKLTMKILEERQGIRSDGGYPFRGNFGY
OMDEMSRFDVVSDQELAAQRYSGNNNOVSLITIGLPHCDSLSSTHHQGFMQTHHGIPIR
RRVKIGETEEYGPATINGGSSTTTAARSSAAAAAANNGMNI ONQKRYVAQLLPDFVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="putative homeodomain transcription factor"
/protein id="AAL59997.1"
/db xref="G1:18176173"
/translation="MAAYFHOVPEISAGSDGGLQTLILMNPTTYVQYTQQDNDSNNN
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VLHGYPPRVQYSLYGSHQVDPTHQQAACETPRAQQGLSLTLSSQQQQQQHHQQHQDPI
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tion is based on the January 2002 version of the Arabidopsis submitted to GenBank.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----AAGTTGCTGTTGAGCTTACAACTGCTCAAAGACAAGAACTTCAAA
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                                                                                                                                                                                                       /clone="RAFL09-25-N04 (R18537)"
/ecotype="Columbia"
/note="This clone is in a modified pBluescript vector
(FLC-1) as a BamHI/XhoI insert."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.9%; Score 324.6; DB 8; Length 2572; 65.2%; Pred. No. 2.5e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches 264; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="At2g35940"
/note="not present in genomic sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="compared to genomic sequence"
/replace="c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="compared to genomic sequence"
                                                                                   1. .2572
/organism="Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=experimental
                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:3702"
                                                             Location/Qualifiers
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/gene="At2g35940"
.2417. .2418
/gene="At2g35940"
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/gene="At2g35940"
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                                                                                                                                                                                               /chromosome="2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 534; Conservative
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The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi, S., Satohk, V., Nagata, T., Kawagashira, N., Doi, K., Kikuchi, S., Satohk, J., Ishiawa, M., Yamada, H., Obda, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Indimura, T., Poundation of Advancement of International Science Genome Sequencing & Analysis Group:, Octomo, Y., Murakami, K., Iida, Y., Sugano, S., Pujimura, T., Suzuki, Y., Teunoda, Y., Kucoaaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yoshamura, A., Miura, J., Kwaui, J., Carninici, P., Adachi, J., Alzawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imctani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Yoshino, M. and Hayashizaki, Y. Saito, R., Shiraki, T., Yoshino, M. and Hayashizaki, Y. Gollection, mapping, and annotation of over 28,000 cDNA clones from Collection, mapping, and annotation of over 28,000 cDNA clones from Collection, Marking M., Missaki, M., Mi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (japonica cultivar-group) cDNA clone:001-044-C01, full Akio4872
                                                                                                              GTGTTGGGGGGTTTGAGGGGTCGAGGTTCGTGGACCACCACTTGAGACACAAA 1305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCAGGTGTCTAACTGGTTCATAAATGCTCGAGTTCGATTATGGAAGCCAATGGTAGAAG 1516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1186 CGATCGCTGGTCAGATAAAAGCGGCCAACAAGAGTCTTGGGGAAGAAGATTCAGTGTCTG 1245
                                                                                                                                                                                                                         1286 GCGCCCTGCAACAGATAGGAATGATGCAAC-----CAAATGCTTGGAGACCCCAAA 1336
                                                                                                                                                                                                                                                                                             GAGCTCTTCAACAACTGGGAATGATTCAACATCCTTCCAATAATGCTTGGAGACCTCAAC 1365
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                --GGAGGGAAAATCGAAGGCTCAAGACTCAAATTTGTGGACCATCATCTAAGGCAACAAC
                                                                                                                                                                                                                                                                                                                                                                                                                               GTGGTCTCCCAGAACGAGCCGTCTCAGTTCTCCGTGCTTGGCTCTTCGAACACTTTCTTC
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                                                                                                                                                                                                                                                                                                                                                                          GAGGITTACCTGAAAGAGCTGTCTCTGTCCTTCGTGCTTTGGCTTTTCGAAGACATTTTTCTTC
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VERSION
KEYWORDS
SOURCE
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AK104872
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OMDEMSRFDVVSDQELMAQRYSGNNNGVSLTLGLPHCDSLSSTHHQGFMOTHHGIPIG
RRVKI GETEEYGPATINGGSSTTTAHSSAAAAAYNGMNI QNQKRYVAQLLPDFVA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1006 TGAAGAAAGCAAAACTTAGTAACATGCTTCATGAGGTGGAGCAGAGATATAGACAGTACC 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1052 ATCACCAAATGCAAATAATTGTATTATCATTTGAGCAAGTAGCAGGAATTGGATCAGCCA 1111
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                                                                                                                                         Nguyen,M, (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W. (SSP/Stanford) contributed equally to this work as PIs. Location/Qualifiers
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/protein_id="AAM20705.1"
/db_xref="GI:20466776"
Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.1
Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P.,
Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tch 11.9%; Score 324.6; DB 8; Length 2578; al Similarity 65.2%; Pred. No. 2.5e-55; 534; Conservative 0; Mismatches 264; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="This clone is in pBluescript"
                                                                                                                                                                                                                                                                                                                                'organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="RAFL09-94-K12 (R25364)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="synonym: F11F19.15"
                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ecotype="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="At2g35940"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene="At2g35940"
                                                                                                                                                                                                                                                                                                                                                                                                                                       'chromosome="2"
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The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Stienki,T., Foundation of Advancement of International Science Genome Sequencing Analysis Group:, Otomo,Y., Murakami,K., Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y., Murakami,K., Kurosaki,T., Kodama,T., Maruda,H., Kobayashi,M., Xie,Q., Lu,M., Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niikura,J., Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Mitka,J., Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN:,
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                                                                                                                                                                                                                     1065 AATAATTGTATTATCATTTGAGCAAGTAGCAGGAATTGGATCAGCCAAATCATACACTCA 1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 302 AGGAATGATGCAACCAAATGCTTGGAGACCCCCAAAGAGGTTTACCTGAAAGAGCTGTCTC 1361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1362 TGTCCTTCGTGCTTGGCTTTTCGAGCATTTTCTTCATCCTTACCCAAAGGATTCAGACAA 1421
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                                                                                   AK12136.1 GI:37990979
FLI_CDNA; CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      715 GATCAATGTTATCAGGAAAAAGCTTGGCGAGGAAGAGAAACTCATCTGGCAAGGAGGAAGAAA 774
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                                                                                                                                                                                                                                                                 895 AATTCTTCGCGCTTGGCTGTTTGAACACTTCCTCCATCCGTACCCAAAAGATTCCGAGAA
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              475 TAATGCAGCACCTGAGCTTTCCACTGCTGAGAAGCAAGAGCTTCAGAACAAAATGGCAAA
                                                                                                                                                    535 ACTGATGGCAATGTTGGATGAGGTGGACCGGAAATACAAGCATTATTACCACCAAATGCA
                                                                                                                                                                                                                                                                                                                                                               1125 ATTAGCTTTGCATGCAATTTCGAAGCAATTCAGATGCCTAAAGGATGCAATTGCTGAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                            655 AGTIGCICITCAGACAATCICACGCCACTITCGGIGCCTGAAGGAIGCIATCAATGAICA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            URL: http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
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                                                                                                                                                                                                                                                                                                                                                                                        Yoshimura, A.

Direct Submission

Submission

Submission

Submission

Submission

Agrobicogleal Sciences, Department of Molecular Genetics, Head of

Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki

305-8602, Japan (E-mail:skikuchi@miss.affrc.go.jp,

Tel:81-29-838-7007, Pas.81-29-838-7007,

This clone is one of the 28K full-length cDNA clones from japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 415
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Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Narikawa, R., Nikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Nosato, N., Otomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sakai, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Takaku, K., Tagami, M., Tagami, Takeda, Y., Tagawa, A., Takakani, F., Tarkku, Lakahira, S., Tanaka, T., Tomaru, A., Toya, T., Tunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCTAAGTATCTGAAAGCTGCACAAGAGCTTCTTGATGAAGTTGTTAATATTGTTGGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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0; Mismatches 339; Indels
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/cultivar="Nipponbare"
/db_xref="taxon:39947"
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Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Salto, R., Sasaki, D., Saco, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M. and Hayashizaki, Y. Collection, mapping, and annotation of over 28,000 cDNA clones from Science 301 (5631), 376-379 (2003)

2869764

MEDLINE PUBMED

JOURNAL

TITLE

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REFERENCE
AUTHORS
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URL: http://cdnaol.dna.affrc.go.jp/cDNA/
NTAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagaahlra,N., Doi,K., Kibhimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,M., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T.,
Yamamoto,M. and Nakahama,Y.
FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y.,
FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y.,
FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y.,
FAIS Genome, Suzuki,Y., Kusumegi,T., Lu,M.,
Kobayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M.,
Ryu,K., Sugano,S., Yoshimura,A., Matsubara,K. and Murakami,K.
Asido,Y. Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K.
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Genomic Science,K.,
Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K.,
Hara,A., Hashizume,W., Hayashida,K., Mayatsu,J., Kouda,M.,
Koya,S., Kurihara,C. Mataywama,T., Miyazaki,A., Murata,M.,
Koya,S., Kurihara,C., Mataywama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Sano,H., Sasaki,C., Sakai,K.,
Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K.,
Takama,Akhahlan,Akhira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K.,
Takamirah,A., and Hayashizaki,Y.
                                                                                                                                                                                                        Submitted (31-JAN-2003) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)
                                                                             3 (bases 1 to 2476)
Kikuchi, S.
from japonica rice
Unpublished
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| Organism="Oryza sativa (japonica cultivar-group)
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                                                                                                                                           Score 295.6; DB 8;
Pred. No. 1.9e-49;
0; Mismatches 339;
                                  /mol_type="mRNA"
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/clone="J023122008"
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Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K. Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adenbi, J., Alzawa, K., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Moril, F., Idda, J., Imamura, K., Imcani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nishi, K., Nomura, K., Numagawi, R., Saicoh, H., Sakai, C., Sakai, K., Sakazume, N., Oho, M., Osato, N., Ota, Y., Zaicoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sakai, C., Sakai, K., Shinagawa, A., Shiraki, T., Takahashi, F., Takaka-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.
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Pred. No. 1.9e-49;
0; Mismatches 339;
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Best Local Similarity 60.3%;
Matches 528; Conservative
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Adachi, J., Alzawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, M., Hayashizaki, Y., Hayateu, M., Hiramoto, K., Hiraoka, T., Horta, I., Iida, Y., Ikeda, R., Imamura, K., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawanata, M., Kakangawa, S., Katoh, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Kodama, T., Kojima, K., Mursakan, T., Murata, M., Mura, J., Miyazaki, A., Mizuho, K., Murakani, K., Murata, M., Nigata, T., Nakamura, M., Namiki, T., Narikawa, R., Nikura, J., Nishi, K., Nomura, K., Nomura, K., Nomura, K., Nomura, K., Nomura, K., Sakazume, N., Caso, H., Osato, N., Cotomo, Y., Satoh, M., Sakai, C., Sakai, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sagabe, Y., Sugano, S., Sugawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and M., Maria, A., Yazaki, J., Yokomizo, S. and M., Maria, A., Yazaki, J., Yokomizo, S. and M., Maria, A., Yazaki, J., Yokomizo, S. and
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NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satch,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Naniki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
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Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice arice 301 (5631), 376-379 (2003)
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Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
205-6602, Japan (E-mail:sKikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007, Fax
                                                                                                                                                                                                                                                                                      AKO70465.1 GI:32980489
FLI CDNA, CAP trapper.
Cryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaa.
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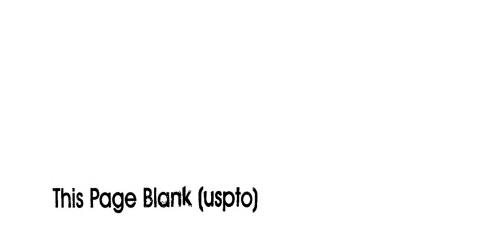
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asterids; lamids; Solanales; Solanaceae; Solanum.
(Chen, H., Rosin, F. M., Prat., S. and Hannapel, D.J.
Interacting transcription factors from the three-amino acid loop extension superclass regulate tuber formation
Plant Physiol. 132 (3), 1391-1404 (2003)
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Submitted (07-AUG-2001) Department of Horticulture, Iowa State
University, 257 Horticulture Hall, Ames, IA S0011-1100, USA
Location/Qualifiers
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/product="BEL1-related homeotic protein 30"
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(bases 1 to 2065)

Chen, H., Rosin, F.M. and Hannapel, D.J.
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/organism="Solanum tuberosum"
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EFNCLDSGNRQQPFWLLPSAT"
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                                                                                                                                      Score 295.2; DB 8;
Pred. No. 2.3e-49;
0; Mismatches 313;
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                                                                                                                                Query Match
Best Local Similarity 61.0<sup>o</sup>
Marches 499; Conservative
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Abz13532 Arabidops	Adb23149 Environme	Add30303 Plant yie	Adi44208 Plant tra	Adq37104 Cell prol	Aac36460 Arabidops	Aac43406 Arabidops	Adg88236 A. thalia	Ado62706 Transcrip	Abk82114 DNA encod	Aac39138 Arabidops	Aad06493 Arabidops	Ado61968 Transcrip	Aac36745 Arabidops	Ado62707 Transcrip	Ado63042 Transcrip	Abz14349 Arabidops	Abz13100 Arabidops	Aad06494 Arabidops	Adc46618 Thalecres
SUMMARIES	ΩI	ABZ13532	ADB23149	ADD30303	ADI44208	ADQ37104	AAC36460	AAC43406	ADG88236	ADO62706	ABK82114	AAC39138	AAD06493	AD061968	AAC36745	ADO62707	AD063042	ABZ14349	ABZ13100	AAD06494	ADC46618
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	& Query Match	11.9	11.9	11.9	11.9	10.2	9.5	9.5	9.5	8.9	8.7	8.6	8.6	8.6	8.6	8.5	8.4	8.5	8.2	8.2	8.2
	Score	324.6	324.6	324.6	324.6	278.8	261	259.4	259.4	244.4	237.6	234.6	234.4	234.4	234.4	231.8	230.2	225.4	224	224	224
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8.2	8.2	8.1	8.1	8.1	8.1	7.8	7.6	7.4	6.8	e. 9	6.8	8.9	9.9	8.9	6.7	6.7	9.9	6.5	6.2	6.1	6.0	5.8	5.8
224	224	222.6	222.6	222.6	222.6	213.4	207	201.4	187.2	187.2	187.2	187.2	187.2	187.2	183.8	182.8	180.4	176.8	170.2	166	164.6	159.8	158
21 22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Arabidopsis thaliana stress regulated gene SEQ ID NO 1337. Arabidopsis thaliana; plant; gene; stress; transgenic; ds. Zhu T; (SCRI) SCRIPPS RES INST. (SYGN) SYNGENTA PARTICIPATIONS AG. BP. Wang X, 24-AUG-2000; 2000US-0227866P. 26-JAN-2001; 2001US-0264647P. 22-JUN-2001; 2001US-0300111P. ABZ13532 standard; DNA; 2043 24-AUG-2001; 2001WO-US026685. (first entry) Arabidopsis thaliana. Kreps J, WPI; 2002-304127/34. WO200216655-A2. 21-JAN-2003 28-FEB-2002. Harper JF, ABZ13532; ABZ13532

Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses. Claim 144; SEQ ID NO 1337; 577pp + Sequence Listing; English.

cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polymuclectides in the plant cell with an array or probes representative of the plant cell genome, and (b) detecting a profile of expressed polymuclectides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants The invention relates to identifying a stress condition to which a plant

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with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
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                                                                                                                                                                               DB 6; Length 2043;
                                                                                                                                     Sequence 2043 BP; 627 A; 507 C; 507 G; 402 T; 0 U; 0 Other;
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Pred. No. 3.8e-64;
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Matches 534; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to novel environmental stress-responsive promoters (ADS2163-ADS2322) from Arabidopsis thalians. The promoters are useful in constructing and breeding stress-resistant plants for applications in agriculture and horticulture. The present sequence was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caattgctgaggaagtaaaggcgaggaggaggtttaggtgaagaggaaggcttg----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    569 TTGTTAGCTCCAAGTACTTGAAGGCAGCACAAGAGCTTCTTGACGAAGTAGTCAACGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      818 TTGGAAAAAGCATCAAAGGAGATGATCAAAAGAAGGATAATTCAATGAATAAAGAATCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGCCTTTGGCTAGTGATGTCAACACTAATAGTTCTGGTGGTGGTGAAAGTAGCAGCAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGAAAAAAGCCAAGCTTCTTGCCATGCTTGAAGAGGTGGAGCAAAGGTACAGGTACC
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                                                  SEO ID 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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65.2%; Pred. No. 3.8e-64;
ive 0; Mismatches 264;
                                               promoter-related
                                                                                                  Plant; environmental stress; promoter; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 10; Page 470-475; 520pp; Japanese
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                                                  stress-responsive
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29-JAN-2002; 2002JP-00020329.
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(first entry)
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CGATCGCTGGTCAGATAAAAGCGGCCAACAAGAGTCTTGGGGGAGGAAGATTCAGTGTCTG 1048
                                                --CAAATGCTTGGAGACCCCAAA 1336
                                                          ATCCATACCCTAAGGATTCGGACAAGCACATGCTAAGCTAAGCAAACAGGACTCACTA 1288
                                                                                                                                                           properties,
.g. growth rate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptides, useful
                --GGAGGGAAAATCGAAGGCTCAAGACTCAAATTTGTGGACCATCATCTAAGGCAACAAC
                                                                                                                                                  GCCAGGTGTCTAACTGGTTCATAAATGCTCGAGTTCGATTATGGAAGCCAATGGTAGAAG
                                                                               GAGGITTACCTGAAAGAGCTGTCTCTGTCCTTCGTGCTTTGGCTTTTCGAGCATTTTCTTC
                                                                                               ATCCTTACCCAAAGGATTCAGACAAAATCATGCTTGCTAAGCAAACGGGGCTAACAAGGA
                                                                                                                                                                                                                                                                                                           ds; transcription factor; transgenic plant; growth rate; senescence; seed germination rate; plant vigor; seedling vigor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heard JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adam LJ, Dubell AT, Heard JE
r TL, Creelman RA, Pineda O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New plant transcription factor polynucleotides and polypep
in producing transgenic plants with commercially valuable
such as an alteration in a plant growth characteristic, e.
or apomixis.
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                                                                                                                                                                                           AGATGTACATGGAGGAAATGAAGGAGCAGGCAAAGAACA 1387
                                                                                                                                                                                   AAATGTACTTGGAAGAAGTGAAGAATCAAGAACAAAACA
                                                                                                                                                                                                                                                                                            Plant yield-related polymucleotide clone G1589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, SEQ ID NO 332; 454pp; English
                                                GCGCGCTGCAACAGATAGGAATGATGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reuber TL,
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19-NOV-2001; 2001US-0336649P.
11-DEC-2001; 2001US-0338692P.
14-JUN-2002; 2002US-00171468P.
                                                                                                                                                                                                                                                                                                                                                                                     09-AUG-2002; 2002WO-US025805
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Riechmann JL,
                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                            CDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jiang C,
                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana
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                                                                                                                                                                                                                                           standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratcliffe O,
Pilgrim ML,
Broun PE;
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producing transgenic plants with commercially valuable properties, i.e. modified or altered desirable traits as compared to a reference plant, such as an alteration in a plant growth characteristic, e.g. growth rate, germination rate of seeds, vigor of plants and seedlings, or leaf and flower senescence. Sequence information related to the polynucleotides and polypeptides can also be used in bioinformatic search methods. The transgenic plant is useful for growing a progeny plant from a parent plant. This sequence represents one of the cDNAs of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                21;
                                                                                                                                                                                                                                                                                                                                       DB 10; Length 2385;
                                                                                                                                                                                                                                                                            Sequence 2385 BP; 748 A; 578 C; 565 G; 494 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                              Score 324.6; DB 10; Length
Pred. No. 4e-64;
0; Mismatches 264; Indels
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Best Local Similarity 65.2°
Matches 534; Conservative
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The invention relates to a number of isolated Arabidopsis thaliana cDNA sequences and their encoded proteins which are especially transcription factor related cDNA's and proteins. The isolated or recombinant plant transcription factor polynucleotides and polypeptides are useful in

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shade avoidance.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention describes a transgenic plant comprising a recombinant polynucleotide of any one of more than 500 nucleotide sequences fully defined in the specification or its complement. The method of the invention can be used to produced a plant having altered traits such as: enhanced tolerance to abiotic stress; glyphosphate tolerance; hormone sensitivity; disease resistance; sugar sensing; early or late flowering; altered flower structure, change in stem bifurcations, altered branching pattern, reduced apical dominance, reduced trichome density; lack of trichomes; reduced apical dominance, reduced trichome density; lack of trichomes; increased root flower; altered stem morphology; increased root growth; increased root hairs; altered seed development; altered cell proliferation or cell differentiation; rapid development; altered cell proliferation or cell differentiation; rapid development; compandature sensesence; increased necrosis; increase in seediling or plant size; decreased plant size; leaf morphology; seed morphology; seed biochemistry; increase in root anthocyanins; increase in plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   t any one
search
                                                                                                                             glyphosphate tolerance; hormone sensitivity; disease resistance, sugar sensing; flowering; flower structure; stem bifurcation; branching pattern; apical dominance; trichome; stem morphology; root prowth; root hair; seed development; cell proliferation; cell differentiation; premature senescence; necrosis; plant size; leaf morphology; seed morphology; seed morphology; seed biochemistry; root anthocyanin; plant anthocyanin; light response; shade avoidance; bioinformatic; transcription factor; ds.
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in bioinformatic searc
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Keddie J,
                                                                                                                   transgenic; plant; enhanced tolerance to abiotic stress;
                                                                                           Plant transcription factor related polynucleotide #1693
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Reuber TL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   r transgenic plant comprising a recombinant more than 500 nucleotide sequences, useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yu G;
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Adam LJ,
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             ВР
             standard; DNA; 2385
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Ratcliffe O,
                                                                 (first entry)
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RIECHMANN J L.
JIANG C.
HEARD J B.
HAAKE V.
CREELMAN R A.
RATCLIFFE O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADAM L J.
REUBER T L.
KEDDIE J.
BROUN P E.
PILGRIM M L.
DUBELL A N.
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P-PSDB; ADI44209.
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Creelman RA,
                                                                                                                                                                                                                                                  Unidentified
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                                                               22-APR-2004
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             ADI44208
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                                                                                                                                                                                                                                                                                                                                     747 TTGTTAGCTCCAAGTACTTGAAGGCAGCACAAGAGCTTCTTGACGAAGTAGTCAACGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                    807 ATTCCGATGACATGAACGCTAAATCCCAACTATTCTCATCGAAAAAGGGTAGTTGCGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 AGTCATACACGTCGCTAGCATTGAAAACCATATCAAGACAGTTCCGTTGCTTGAAAGAGG
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                                                                                                                                                                                                                                                                                                                                                                                     818 TTGGAAAAGCATCAAAGGAGATGATCAAAAGAAGGATAATTCAATGAATAAAGAATCAA
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                                                                                                                                                                                                                                21; Gaps
                                                                                                                                                                         Score 324.6; DB 12; Length 2385;
Pred. No. 4e-64;
0; Mismatches 264; Indels 21;
anthocyanins, or alteration in light response or shade avoidan transgenic plant, polynucleotides and polypeptides are useful bioinformatic search methods. This sequence represents a plant transcription factor related polynucleotide.
                                                                                                                               Sequence 2385 BP; 748 A; 578 C; 565 G; 494 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1517 AAATGTACTTGGAAGAAGTGAAGAATCAAGAACAAAACA 1555
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                                                                                                                                                                              11.9%;
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Best Local Similarity 65.2
Matches 534; Conservative
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  1182 AATTCTTCGTGCTTTGGCTTTTTTGAACACTTCCTTCACCCGTATCCAAAGATTCAGAAA 1241
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                                                                                                                  1062 ATTAACGCGCCTCCGTTATATTGACCAGCAATTAAGACAACAGCGCGCTTTCCAGCAGTA 1121
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                                                                             CTCAA---GACTCAAATTTGTGGACCATCATCTAAGGCAACAACGCGCGCTGCAACAGAT
                                                                                                                                                                                             1122 TGGTTTGTTACAGCAAAATGCTTGGAGGCCACAGAGGGGACTGCCGGAAACTCAGTTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                     AGGAATGATGCAAACCTTGGAGACCCCCAAAGAGGTTTACCTGAAAGAGCTGTCTC
                                                                                                                                                                                                                                    TGTCCTTCGTGCTTGGCTTTTCGAGCATTTTCTTCATCCTTACCCAAAGGATTCAGACAA
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990S-0123548P-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to an isolated nucleic acid molecule encoding a cell proliferation-related polypeptide. The nucleic acid molecule and the encoded polypeptide, and methods are useful for modulating cell proliferation, senescence, differentiation, development, and stress response in plants, and for producing enhanced food crops. The present sequence represents a cell proliferation-related nucleic acid sequence. The present sequence is published separately from the main body of the specification as EPO data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           945 TGAAGTTGCTGTTGAGCTTACAACTGCTCAAAGACAAGAACTTCAAATGAAAAAAGCCAA 1004
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                                                                       cell proliferation related polypeptide; cell proliferation; senescence; differentiation; stress response; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid molecule encoding a cell proliferation-related polypeptide, useful for modulating cell proliferation, senescence, differentiation, development, and stress response in plants, and for producing enhanced food crops.
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                                    Cell proliferation-related nucleic acid sequence #132
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06- MAY - 1999; 14- MAY - 1999; 16- UN - 1999; 16- UN - 1999; 16- UN - 1999; 16- UN - 1999; 18- UN - 1999; 19- UN -	1-JUL-1999 1-JUL-1999
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                    Arabidopsis thaliana DNA fragment SEQ ID NO: 39140
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9905-0123180P.
9905-012548P.
9905-012564P.
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 17-OCT-2000 (first entry)
                                                                            Arabidopsis thaliana
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  TGCTGTTGAGCTTACAACTGCTCAAAGACAAGAACTTCAAATGAAAAAAGCCAAGCTTCT 1010
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Pred. No. 1.5e-49;
0; Mismatches 200; Indels
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                                                                                                                                                                                CATGCTTGCTAAGCAAACGGGGCTAACAAGGAGCCAGGTGTCTAACTGGTTCATAAATGC 1484
                                                                                                                                                                                                                                                                                                                                                     Pathogen infection-related gene; plant; Peronospora parasitica; defence mechanism; RPP4; pathogen resistance; transgenic plant; oomycete; fungus; bacterium; virus; nematode; insect; aphid; gene; ss.
717 GGTGATAAGGAAAAGTTTAGGAGGGAACAGGATGCATCAGATGGAGAGGAGGAGTGGGAT 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to 691 Arabidopsis thaliana genes (ADC87559--ADG87557}) whose expression is altered in response to pathogen infection, and to homologues of these genes from other plants or fungi, especially from maize, soybean, barley, alfalfa, sunflower, canola (oilseed rape),
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a pathogen.
                             777 AAGCAGGTTAAGGAATGTTGATCAACAGGTAAGGCAACAAGAGCGTTGCAGGTTAGG
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UNIV NORTH CAROLINA.
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EULGEM T.
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Arabidopsis plants infected with the comycete Perconospora parasitica, Arabidopsis plants infected with the comycete Perconospora parasitica, indicating that they play a role in defence mechanisms. The genes of the invention are regulated by RPP7 or RRPB which act via unconventional signalling cascades, or by the RPP4-dependent pathway. The invention also relates to polyapstides encoded by the pathogen infection-related genes; promoter motifs from pathogen of pathogen resistant transgenic of lants and their progeny comprising a polynucleotide of the invention; and a method of identifying a plant cell infected with a pathogen. The polynucleotide sequences and methods of the invention are useful for identifying plants infected with a pathogen, and for conferring resistance to pathogens such as comycetes, fungi, bacteria, viruses, namotodes and insects (e.g., aphids). The present sequence represents an example and insects (e.g., aphids). The present sequence represents and relations gene whose expression is altered in response to Peronospora parasitica infection. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to novel plant transcription factor proteins (I) and nucleotide sequences (II) (ADO61534-ADO63778). The sequences can be used to produce transgenic plants, which overexpress (II), where the transgenic plant has an altered trait as compared to a non-transgenic plant or wild-type plant. The transgenic plant comprises can altered trait selected from increased tolerance to abloid stress, increased tolerance to cold, increased tolerance to cold, increased tolerance to cold, increased tolerance to heat, increased colerance to pearly increased tolerance to cold, increased tolerance to heat, increased tolerance to pearly in heat, increased tolerance to low phosphate conditions, increased tolerance to disease, including fungal disease and particularly Erysiphe, Fusarium and Botryvis, increased tolerance to multiple fungal pathogens, increased tolerance to multiple fungal pathogens, increased tolerance to multiple fungal pathogens, increased tolerance to colditions, increased tolerance to multiple fungal pathogens, increased tolerance to multiple fungal pathogens, increased tolerance to colditions, increased tolerance to multiple fungal pathogens, increased tolerance to sugars, altered dioven functions estructure, loss of flower determinacy, altered flower structure, loss of flower determinacy, altered shoot meristem development, altered branching pattern, altered trichome structure, altered valued seed trichome structure, altered call development, altered call development, altered call development, altered call development, altered call death, fast growth, fast growth, altered call defending in leaf shape, increased biomass, large seedlings, dwarfed plants, dathogen in leaf shape, increased leaf shape, increased large, altered senenced altered senescence, abnormal energy leaves, altered senesce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   altered seed coloration, altered seed size, altered seed shape, large, seed, increased leaf wax, increased leaf fatty acids, altered seed oil content, altered seed protein content, altered seedprenyl content, altered leaf prenyl lipid content, increased anthocyanin levels, and decreased anthocyanin levels. Note: The sequence data for this patent did
                                                                                                                                                                                                                                                                                                 Plant; transcription factor; transgenic plant; abiotic stress tolerance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptides, useful for producing transgenic plants with advantageous
properties compared to a reference plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reuber TL;
                                                                                                                                                                                                                                                                                                                             osmotic stress tolerance; cold tolerance; heat tolerance; low nitrogen tolerance; low phosphate tolerance; fungal disease; glyphosate resistance; flowering; fertility; seed development; ds
                                                                                                                                                                                                                                   Transcription factor G2550 orthologous sequence, SEQ ID 1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         recombinant polynucleotide encoding transcription factor
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Sherman BK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 1173; 510pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MEND-) MENDEL BIOTECHNOLOGY INC.
                               ADO62706 standard; DNA; 1971 BP
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                                                                                                                                                                     (first entry)
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Riechmann JL, Haake
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                                                                                                                                                                                                                                                                                                                                                                       201 AGGCTCGAGCAACAATGTCTTGAACTCACAATACCTCAAGGCAGCACAGGAGTTGCTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                    801 TGAAGTTGTTAATATTGTTGGAAAAGCATCAAAGGAGATGATCAAAAGAAGGATAATTC
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                                                                                                                                                                                                                                                    Gарв
                                                                                                                                                                                   DB 12; Length 1971;
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      but was obtained
                                                                                                                          T; 0 U; 0 Other;
                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                Match 8.9%; Score 244.4; DB 12; Local Similarity 57.7%; Pred. No. 9.9e-46; les 512; Conservative 0; Mismatches 346;
not form part of the printed specification, electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                          Sequence 1971 BP; 667 A; 360 C; 451 G; 493
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Sequence 706 BP; 210 A; 148 C; 188 G; 147 T; 0 U; 13 Other;

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DNA encoding novel floral meristem identity protein LpHBb.
ABK82114 standard; cDNA; 706 BP
          (first entry)
                                                                                      WPI; 2002-454601/
P-PSDB; ABG60937
                                             Lolium perenne.
                                                                                Spangenberg G,
                                                  WO200233091-A1
          27-AUG-2002
                                                        25-APR-2002
                                                                        (AGRI-)
                                                                           (AGRE-)
                                                                                                      phases
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The invention describes a substantiality purities of substance to the invention describes a substantiality purities or in the invention describes a substantiality burities or the invention of the substantiality of the proteins, foreins, APETALA2 (AR2) and AP2-like proteins, Homeo-box proteins (HB) and HB-like proteins, or their functionally active fragments or variants. Condition or their functionally active fragments or variants. Nucleic acid (II) encoding (II), is useful for modifying plant life cycles and/or growth phases, flowering processes, flowering and/or plant architecture and/or flower and/or inflorescence development in a plant, which involves introducing (II), (III) or (IV) into the plant. The carchitecture and/or flower and/or inflorescence development in a plant, which involves introducing (II), (III) or (IV) into the plant. The carchitecture and/or flower and/or flower and seed development, e.g., enhance activities may alter flower, embryo and seed development, e.g., enhance activities may alter flower, embryo and seed development, e.g., enhance activities may alter flower, enbryo and seed development, e.g., enhance of individual or simultenesses of one floral organ in another. Manipulation of CEN or inhibit embryo differentiation and growth or alter flower organ identity of the number of leaves made before flowering.

Considering time and the number of leaves made before flowering in dentity conversion of one floral organ in another. Leads to a change in through conversion of one floral organ in another. Manipulation of flowering plant architecture has a wide range of applications such as: inducing male sterility for hybrid seed production; changing plowering in forgate grasses thus stopping the formation of less digestible stems and increasing branching to enhanced business in fruit trees; altering plant statures, and in blocking flowering and reducing release for allergenic pollen. This sequence encodes a novel floral carget for manipulating plant life cycles Ryegrass; fescue; MADS-box; MADS: MADS-like protein; CENTRORADIALIS; CEN, CEN-like protein; APETALA2; AP2; AP2-like protein; HB; Homeo-box protein; HB-like protein; plant growth; plant architecture; inflorescence development; flower development; embryo development; seed development; flower organ identity; phase change; male sterility; hybrid seed production; herbage quality; early maturing crop; blomass increase; branching increase; blocking flowering; invention describes a substantially purified or isolated polypeptide New substantially purified or isolated polypeptide e.g., MADS-box, CENTRORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass or fescue species, useful for controlling plant life cycles and/or growth allergenic pollen; floral meristem identity protein; gene; ss Emmerling M; AGRIC VICTORIA SERVICES PTY LTD AGRESEARCH LTD. Ong EK, Claim 6; Fig 41; 290pp; English. Sawbridge II, 17-OCT-2001; 2001WO-AU001311. 19-OCT-2000; 2000AU-00000873. 2002-454601/48.

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947 AAGTTGCTGTTGAGCTTACAACTGCTCAAAGACAAGAACTTCAAATGAAAAAAGCCAAGC 1006
                                                                                                                                                                                                                            1127 TAGCTTTGCATGCAATTTCGAAGCAATTCAGATGCCTAAAGGATGCAATTGCTGAGCAAG 1186
                                                                                                                                                                                                                                                                                     1187 TAAAGGCGACGAGCAAGAGTTTAGGT---GAAGAGAAGGCTTGGGAGGGAAAATCGAAG 1243
                                                                                                               1067 TAATTIGTATTATCATTIGAGCAAGTAGCAGGAATTIGGATCAGCCAAATCATACACTCAAAT 1126
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                                                                                  173 ATGCTGTACCTGAGCTTTCCACTGCTGAGAAGCAAGAACTTCAGAACCAAGATGGCCAAAC 232
                                                                                                                                  293 ATGTGGTTTCATCTTTTGATGTGGTGGCTGGGATCTGCAAAGCCGTACACTGCAG 352
                                                                                                                                                                                                                                                                                                               593 TTCTCCGTGCTTGGCTTTTCGAACACTTCCTTCACCCGTACCCAAAAGATTCAGAAAAGT 652
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                            Indels
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Score 237.6; DB 6;
Pred. No. 2.5e-44;
0; Mismatches 174;
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99US-0123180P.
99US-0125548P.
99US-0126264P.
99US-0126762P.
99US-0127462P.
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Query Match
Best Local Similarity 66.7
Matches 355; Conservative
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01-APR-1999;
06-APR-1999;
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1251 AGACCTCAAAGAGGTCTTCCTGAAAACTCTGTTTCTGTTCTCCGTGCTTGGCTCTTCGAA 1310
                                                                                         CTAACAAGGAGCCAGGTGTCTAACTGGTTCATAAATGCTCGAGTTCGATTATGGAAGCCA 1506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is a cDNA encoding Arabidopsis thaliana transcription factor homologue. The transcription factors are used to alter the structure and developmental characteristics of plants such as soybean, wheat, corn, potato, cotton, rice, oilsed rape, sunflower, alfalfa, sugarcane, turf, banana, blackberry, blueberry, strawberry, raspberry, carrot, cantaloupe, cauliflower, cucumber, coffee, eggplant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thaliana transcription factor homologue"
                                Reuber L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding plant transcription factor polypeptides, for altering the pathogen resistance characteristics of plants, corn, potato and cotton plants.
                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana G418 transcription factor homologue, G2550
                                                                                                                                                                                                                                                                                                                                                                                         Transcription factor; pesticidal; antimicrobial; gene therapy; pathogen tolerance; trichome structure; callose induction; phytoalexin induction; plant structure; plant development; ss.
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RATCLIFFE O.
CREELMAN R.
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P-PSDB; AAE02524.
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PINEDA O.
REUBER L.
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(PINE/)
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(ADAM/)
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0; Mismatches 309; Indels
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grapes, mango, lettuce, honeydew, melon, onion, papaya, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, peas, watermelon, rosaceous fruits and vegetable brassicas. The transcription factors are specifically useful for modifying traits associated with plant's pathogen tolerance such as alterations in cell wall composition, trichome number or structure, callose induction, phytoalexin induction, and alterations in the cell death response. Transgenic plants expressing these transcription factors are more tolerant to biotrophic or necrotrophic pathogens such as fungi, bacteria, mollicutes, viruses, nemaçodes and parasitic higher plants. The transcription factors are also
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                                                                                                                                                                                                                                                                                             Sequence 1575 BP; 512 A; 323 C; 323 G; 417 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                61.6%; Pred. No. 1.8e-43; ive 0; Mismatches 241; Indels
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Matches 392; Conservative
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Transcription factor G2550 coding sequence, SEQ ID 435.
                 ADO61968 standard; DNA; 1575
                                                 (first entry)
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germination in heat, increased tolerance to disease, including increased tolerance to low mitrogen conditions, increased tolerance to low phosphate conditions, increased tolerance to low phosphate conditions, increased tolerance to multiple fungal pathogens, increased resistance to increased disease and particularly Erysiphe, Fusarium and Botrylis, concreased consitivity to ABC, altered sugar sensing, increased tolerance to sugars, increased resistance to glyphosate, increased sensitivity to ABC, altered sugar sensing, increased tolerance to increased sensitivity to ABC, altered sugar sensing, increased tolerance to sugars, altered carbon/nitrogen sensing, early flowering, latered flower structure, loss of flower determinacy, reduced fertility, altered shoot meristem development, altered branching pattern, altered stem morphology, altered vascular tissue structure, reduced apical dominance, altered vascular tissue structure, reduced apical dominance, altered density, altered branching pattern, altered trichome structure, altered vascular tissue structure, reduced avoidance, altered seed development, altered cell differentiation, altered seed development, altered seed development, altered seed reportaning altered seed cell proliferation, altered cell differentiation, altered seed coloration, altered seed some cross patterns, increased plants state, increased blomess, large seedlings, dwarfed plants, dark crossed leaf seed coloration, altered seed site and mass, light creased leaf seed coloration, altered seed site, altered seed coloration, altered seed size, altered seed seed shape, altered seed content, altered seed coloration, altered seed size, altered seed shape, large content, altered seed coloration, altered seed size, altered seed shape, and decreased anthocyanin levels. Note: The sequence data for this patent did decreased anthocyanin levels. Note: The sequence data for this patent did content, increased approach in crossed specification, but was obtained in the sequence data for this patent did not form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to novel plant transcription factor proteins (I) and nucleotide sequences (II) (ADO61534-ADO63778). The sequences can be used to produce transgenic plants, which overexpress (II), where the transgenic plant has an altered trait as compared to a non-transgenic plant or wild-type plant. The transgenic plant comprises an altered trait selected from increased tolerance to abiotic stress,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New recombinant polynucleotide encoding transcription factor polypeptides, useful for producing transgenic plants with advantageous properties compared to a reference plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               increased
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Plant; transcription factor; transgenic plant; abiotic stress tole sencits stress troleance; cold tolerance; heat trolerance; old tolerance; heat tolerance; low nitrogen tolerance; low phosphate tolerance; fungal disease; glyphosate resistance; flowering; fertility; seed development; ds.
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Sherman BK;
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61.6%; Pred. No. 1.8e-43;
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Haake V, Dubell AN,
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17-DEC-2002; 2002US-0434166P.
24-APR-2003; 2003US-0465809P.
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P-PSDB; ADO61969.
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                                                      670 GAGTIGICICCTICAGAACGICAGGAGCIACAGAGCAAGAGAGCAAGCITITAACAATG 729
                                                                                                    Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                           GAGCTTACAACTGCTCAAAGACAAGAACTTCAAATGAAAAAAGCCAAGCTTCTTGCCATG
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 0; Mismatches 241; Indels
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Length 1824; Indels 1137

816

1018 CTTGAAGAGGTGGAGCAAAGGTACAGACAGTACCATCACCAAATGCAAATAATTGTATTA 1077

TCATTTGAGCAAGTAGCAGGAATTGGATCAGCCAAATCATACACTCAATTAGCTTTGCAT

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958 GAGCTTACAACTGCTCAAAGACAAGAACTTCAAATGAAAAAAAGCCAAGCTTCTTGCCATG

Query Match 8.6%; Score 234.4; DB 3; Best Local Similarity 61.6%; Pred. No. 1.9e-43; Matches 392; Conservative 0; Mismatches 241;

1138 GCAATTTCGAAGCAATTCAGATGCCTAAAGGATGCAATTGCTGAGCAAGTAAAGGCGACG 1197

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1198 AGCAAGAGTITAGGTGAAGAGAAGGCTTGGGAGGGAAAATCGAAGG---CTCAAGACTC 1254

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AAATTTGTGGACCATCATCTAAGGCAACAACGCGCGTGCAACAGATAGGAATGATGCAA 1314 AGGTACTTAGÁTCAACGGTTGAGACAACAGAGCTTTGCATCAACAACTTGGAATGGTT 1056 1434

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AAGCAAACGGGGTAACAAGGAGCCAGGTGTCTAAAAAAAGCTCGAGTTCGA

TTATGGAAGCCAATGGTAGAAGAAATGTACTTGGAAGAAGTGAAGAATCAAGAAAC 1554

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to novel plant transcription factor proteins (1) and nucleotide sequences (11) (AD061534-AD063778). The sequences can be used to produce transgenic plants, which overexpress (11), where the transgenic plant has an altered trait as compared to a non-transgenic plant or wild-type plant. The transgenic plant comprises increased tolerance to abiotic stress, increased tolerance to cold, increased tolerance to cold, increased tolerance to cold, increased tolerance to cold, increased tolerance to deet increased tolerance to low introgen conditions, increased tolerance to increased tolerance to low introgen conditions, increased tolerance to low phosphate conditions, increased tolerance to sugars, increased tolerance to multiple fungal pathogens, increased tolerance to glyphosate, increased sensitivity to ABA, reduced sensitivity to ACC, altered sugar sensing, increased tolerance to sugars, altered carbon/nitrogen sensing, early flowering, latered carbon/nitrogen sensing, early flowering, altered flower structure, loss of flower determinacy, and tered and partichome development, altered trichome structure, altered vascular tissue structure, reduced apical dominance, altered development, altered cell proliferation, altered cell expansion, altered cell proliferation, altered cell expansion, altered cell expansion, altered seed cell proliferation, altered cell expansion, altered seed cell expansion, altered seed cell expansion, altered cell expansion, altered cell expansion, altered cell expansion altered seed c
CTATGGAAACCAATGATTGAAGAGATGTATAAAGAAGAGTTTGGAGAATCAGCAGAGTTA 1296
                                                                                                                                                                                                                                                                               Plant; transcription factor; transgenic plant; abiotic stress tolerance;
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Sherman BK;
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                                                             CTCTCTAACTCTAACACACCAAAAAAATGCAG 1332
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Keddie JS,
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V, Dubell AN,
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17-DEC-2002; 2002US-0434166P.
24-APR-2003; 2003US-0465809P.
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Riechmann
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                                green leaves, change in leaf shape, increased leaf size and mass, light green or gray leaves, glossy leaves, altered abaxial/adaxial polarity, altered seed size, altered seed size, altered seed only seed increased leaf fatty acids, altered seed only content, altered seed protein content, altered seed protein content, altered seed protein content, increased anthocyanin levels. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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plant size, increased biomass, large seedlings,
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Search completed: July 29, 2005, 08:33:46 Job time: 1419 secs

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Local Similarity
US-09-640-211A-77
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1: /cgn2_6/ptodatea1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodatea1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodatea1/ina/6A_COMB.seq:*

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US-09-640-211A-1854

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US-09-640-211A-1859

US-09-640-211A-124

US-09-640-211A-124

US-09-640-211A-124

US-09-640-211A-124

US-09-640-211A-137

US-09-640-211A-139

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Maximum Match 100%
Listing first 45 summaries
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                 Sequence 5219, Ap
Sequence 648, App
Sequence 15940, A
Sequence 1031, Ap
Sequence 381, App
Sequence 22, Appl
Sequence 22, Appl
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Sequence 1378, A
Sequence 1259, A
Sequence 12699, A
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Sequence 168053,
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   1357, Ap
5219, Ap
628, App
12776, A
15940, A
1031, Ap
1311, Ap
13145, A
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; Sequence 77, Application US/09640211A
; Patent No. 683446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Composition of Gene Transcription
; FILE REPERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FASESEQ for Windows Version 4.0
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US-09-902-540-1357
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Pred. No. 2.6e-37;
0; Mismatches 67
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US-09-640-211A-1578
; Sequence 1578, Application US/09640211A
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US-09-640-211A-418

Sequence 418, Application US/09640211A

Patent No. 6833446

GENERAL INFORMATION:

APPLICANT: Wood, Marion

APPLICANT: Shenk, Marthew

APPLICANT: Glenn, Matthew

TITLE OF INVENTION: Compositions and Methods for the

TITLE OF INVENTION: Composition of Gene Transcription

FILE REPERENCE: 11000.1021C1U

CURRENT APPLICANTON NUMBER: US/09/640,211A

CURRENT FILING DATE: 2000-08-16

NUMBER OF SEQ ID NOS: 2368

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 418

LENGTH: 323

LENGTH: 323
                                                                                               APPLICANT: Shork, Michael A.
APPLICANT: Shork, Michael A.
APPLICANT: Glenn, Matthew
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REPRENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT APPLICATION NUMBER: 2000-08-16
NUMBER OF SEQ ID NOS: 2168
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (1)...(343)
OTHER INFORMATION: n = A,T,C or G
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; Patent No. 6833446
; GENERAL INFORMATION:
A PAPLICANT: Wood, Marion
A APPLICANT: Shenk, Michae
A APPLICANT: McGrath, Anne
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; ORGANISM: Pinus radiata
US-09-640-211A-418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Pinus radiata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 GAAGAAAA 309
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                                                                                                                                                                                                                                                                                                                                                                 195 GAAGTCAGGTATCAAATTGGTTTATAAATGCCAGGGTTAGACTATGGAAGCCCATGGTGG 254
                                                                                                                                                                 74
                                                                                                                                                                                                                                                      AGAGAGGACTTCCTGAACGCTCTGTTCTGTTCTTCGTGCATGGTTGTTTGAGCATTTTTC
                                                                                                              1274 TAAGGCAACAACGCGCGCGCTGCAACAGATAGGAATGATGCAACCAAATGCTTGGAGACCCC
                                                                                                                                                                 15 TACGACAACAGCGCCCATTTCACCACTTAGGATTGATGGAGCAGCACCCTTGGCGACCGC
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Length 323;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: McGrath, Annette
APPLICANT: Gleath, Annette
APPLICANT: Gleath, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REPERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT APPLICATION NUMBER: US/09/640,211A
SOFTWARE: FastSEO for Windows Version 4.0
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                                                        Indels
                                                        72;
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  DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      255 AGGAGATGTACATGGAAGAACTCAAGGAAGAAAA 289
Score 159.8; DB 4
Pred. No. 3.1e-31;
0; Mismatches 72
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; GENERAL INFORMATION:
  Query Match
Best Local Similarity 73.8%;
Matches 203; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; SEQ ID NO 1854
; LENGTH: 316
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-640-211A-1854
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1054 CACCAAATGCAAATAGTATTATCATTTGAGCAAGTAGCAGGAATTGGATCAGCCAAA 1113
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                             850 TTGGAACACCGGAATCAAAGCTGAGATGCTGAAGAAGGCCAGCGGCCAAAGTAA---- 904
                                                                                                                                                                                     875 CAATGCCTTTGGCTAGTGATGTCAACACTAATAGTTCTGGTGGTGGAAAGTAGCAGCA 934
                                                                                                                                                                                                                                  TGGTTTTAGGCTCTAAGTATCTGAAAGCTGCACAAGAGCTTCTTGATGAAGTTGTTAATA 814
                                                                                         815 TTGTTGGAAAAAGCATCAAAGGAGATGATCAAAAGAAGGATAATTCAATGAATAAAGAAT 874
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                                                                                                                                                                                                                                                                               935 GGCAGAAAAATGAAG-TTGCTGTTGAGCTTACAACTGCTCAAAGACAAGAACTTCAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1234 AAAATCGAAGGCTCAAGACTCAAATTTGTGGACCATCATCTAAGGCAACAACGCGCGCTG
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Sequence 102, Application US/09640211A

Patent No. 6833446

APPLICANT: Word, Marion

APPLICANT: McGrath, Annette

APPLICANT: Glenh, Mathew

TITLE OF INVENTION: Compositions and Methods for the

TITLE OF INVENTION: Modification of Gene Transcription

FILE REFERENCE: 11000.1021C1U

CURRENT APPLICATION NUMBER: US/09/640,211A

CURRENT FILING DATE: 2000-08-16

NUMBER OF SEQ ID NOS: 2368

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 65.64; Pred. No. 1.4e-24;
Matches 196; Conservative 0; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
CRGANISM: Eucalyptus grandis
US-09-640-211A-102
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                             US-09-01-11.11.7-339

| Sequence 359, Application US/09640211A
| Patent No. 6833446
| GENERAL INPORMATION:
| APPLICANT: Wood, Marion
| APPLICANT: Shenk, Michael A.
| APPLICANT: Glenn, Matthew
| APPLICANT: Glenn, Matthew
| TITLE OF INVENTION: Compositions and Methods for the
| TITLE OF INVENTION: Modification of Gene Transcription
| FILE REFERENCE: 11000.102.ClU
| CURRENT APPLICATION NUMBER: US/09/640,211A
| CURRENT FILING DATE: 2000-08-16
| NUMBER OF SEQ ID NOS: 2368
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 65, Application US/09640211A

Batent No. 6833446

GENERAL INFORMATION:

APPLICANT: Wood, Marion

APPLICANT: McGrath, Annette

APPLICANT: McGrath, Annette

TITLE OF INVENTION: Compositions and Methods for the

TITLE OF INVENTION: Modification of Gene Transcription

FILE REFERENCE: 11000.1021C1U

CURRENT APPLICATION NUMBER: US/09/640,211A

CURRENT FILING DATE: 2000-08-16

NUMBER OF SEQ ID NOS: 2368

SOFTWARE: FastSEQ for Windows Version 4.0
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59.4%; Pred. No. 7.6e-25;
ve 0; Mismatches 168; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 5.7%; Score 155.8; DB 4
Best Local Similarity 73.4%; Pred. No. 4.1e-30;
Matches 199; Conservative 0; Mismatches 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 TGTGGAGGAACAAGGAGGCAGAAGTAGAC 271
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Best Local Similarity 59.4%;
Matches 280; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Pinus radiata
              .09-640-211A-359
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US-09-640-211A-1246
; Sequence 1246, Application US/09640211A
; Patent No. 6833446
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Best Local Similarity 80.2%;
Matches 142; Conservative
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  ORGANISM: Eucalyptus grandis
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US-09-640-211A-400
        i OKCANACATO III
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1354 GCTGTCTCTGTCCTTCGTGCTTTGGCTTTTCGAGCATTTTCTTCATCCTTACCCAAAGGAT 1413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132 CACCAGATGGGCATGATGGACGAAGGCCTGGAGGCCGCAGCGGGCCTGCCGGAGCGG 191
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252 GCTGATAAGCATCTGTTGGCTCGACAGACTGGTCTCTCCAGAAACCAGGTCTCGAATTGG 311
                                                      1474 TTCATAAATGCTCGAGTTCGATTATGGAAGCCAATGGTAGAAAAAGTGTACTTGGAAGA 1532
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                                                                                            312 TTCATAAATGCCAGGGTCCGGTTGTGGAAACCCATGGTGGAGGAGATGTACCAGCAAGA 370
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US-09-640-211A-111
; Sequence 111, Application US/09640211A
; Patent No. 683346
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: Grath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Transcription
; TITLE OF INVENTION: Modification of Gene Transcription
; FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SEQ ID NO: 111
; LENGTH: 380
                                                                                                                                                                                                                                   Sequence 1472, Application US/09640211A

Sequence 1472, Application US/09640211A

Patent No. 683346

GENERAL INFORMATION:

APPLICANT: Wood, Marion

APPLICANT: McGrath, Annette

APPLICANT: Glenn, Matthew

TITLE OF INVENTION: Compositions and Methods for the

TITLE OF INVENTION: Modification of Gene Transcription

FILE REFERENCE: 11000.1021GLU

CURRENT FAPLICANTION NUMBER: US/09/640,211A

CURRENT FILING DATE: 2000-08-16

NUMBER OF EEQ ID NOS: 2368

SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 1.4e-24;
0; Mismatches 103; Indels
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Best Local Similarity 65.6%;
Matches 196; Conservative
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US-09-640-211A-1472
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                                                                                                                                                                                                                                                                           61 ACAGACAGGCTCACTAGAAGCCAGGTGTCGAATTGGTTTATAAATGCTCGAGTTCGGCT 120
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Pred. No. 3.4e-21;
0; Mismatches 35; Indels
      Length 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: Shenk, Michael A.
APPLICANT: Morath, Annette
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021C1U
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SEQ ID NO 1246
LENGTH: 380
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Patent No. 6833446

GENERAL INFORMATION:
APPLICANT: Shenk, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: McGrath, Annette
APPLICANT: McGrath, Annette
APPLICANT: McGrath, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
                                                             35; Indels
Query Match
4.4%; Score 121; DB 4;
Best Local Similarity 80.2%; Pred. No. 3.4e-21;
Matches 142; Conservative 0; Mismatches 35.
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1444 GGGCTAACAAGGAGCCAGGTGTCTAACTGGTTCATAAATGCTCGAGTTCGATTATGGAAG 1503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GGCTTGACAAGAAGTCAGGTCTCGAATTGGTTCAATGCAAGAGTGCGTCTCTCTGGAAA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GAGCATTTTCTTCATCCTTACCCAAAGGATTCTGACAAAATCCTGCTTGCAAGGCAGACA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 366;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Word, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: Shenk, Michael A.
APPLICANT: McGrath, Annette
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021CIN
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 57
LENGTH: 474
                                                                                                                                                                                          APPLICANT: Shenk, Michael A.
APPLICANT: Shenk, Michael A.
APPLICANT: Shenk, Annette
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021CLU
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 1241
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Pred. No. 4e-17;
0; Mismatches 36;
       655 CAACCCGTAAAAGTCTCGGAGAGACACCT 687
                                                                                                                   Sequence 1241, Application US/09640211A patent No. 6833446; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 57, Application US/09640211A; Patent No. 6833446
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Best Local Similarity 77.9%;
Matches 127; Conservative
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US-09-640-211A-1241
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US-09-640-211A-57
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                                                                                                        US-09-640-211A-1241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    953 CTGTTGAGCTTACAACTGCTCAAAGACAAGAACTTCAAATGAAAAAAGCCAAGCTTCTTG 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1073 TATTATCATTTGAGCAAGTAGCAGGAATTGGATCAGCCAAATCATACACTCAATTAGCTT 1132
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                                                                                                                                                                                                                                                                                                                            624 GATGCAAATCGTTGTTTCATCGTTTGAGACCGCAGCTGGATTTGGGGCTGCCAAGACATA 683
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4.1%; Score 111.4; DB 4; Length 698;
Best Local Similarity 63.0%; Pred. No. 1.4e-18;
Matches 172; Conservative 0; Mismatches 101; Indels 0
                                                                                                                                                                                                    Length 690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 37, Application US/09640211A

Patent No. 6833446

GENERAL INFORMATION:
APPLICANT: Words. Marion
APPLICANT: McGrath, Annette
APPLICANT: Glenh, Mathew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                40; Indels
                                                                                                                                                                                               4.4%; Score 120; DB 4; 78.3%; Pred. No. 8.4e-21; tive 0; Mismatches 40
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NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 400
LENGTH: 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Eucalyptus grandis
                                                                                                                                                                                                                                             Matches 144; Conservative
                                                                                                 TYPE: DNA
ORGANISM: Pinus radiata
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACT 687
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US-09-640-211A-37
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186 GTGTCTAACTGGTTCATCATCAACGCTCGGGTTCGCCTCTGGAAGCCCCATGGTCGAAGAAATG 245
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                                                            RESULT 15
US-09-640-211A-1399/c
; Sequence 1399, Application US/09640211A
; Sequence 1399, Application US/09640211A
; Patent NO. 683346;
; GENERAL INFORMATION:
; APPLICANT: Shenk, Michael A.; APPLICANT: Shenk, Michael A.; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Transcription
; FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEC 1D NOS: 2368
; SOFTWARE: FastSEC for Windows Version 4.0
; REMOGRANT AND 1399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: July 29, 2005, 14:20:30 Job time : 449 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Eucalyptus grandis
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11337, Ap 153, App 2671, App 335, App 9882, App 7028, Ap 11007, A 31585, A 31585, A

Sequence 3 Sequence 9 Sequence 7

Sequence Sequence Sequence

Sequence Sequence Sequence

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Sequence 130628, Application US/10424599
; Sequence 130628, Application US/10424599
; Sequence 130628, Application No. US20040031072A1
; GENERAL INFORMATION:
    APPLICANT: La Rosa Thomas J
    APPLICANT: Zhou Yihua
    APPLICANT: Zhou Yihua
    APPLICANT: APPLICANT: APON With
    TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
    TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
    TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
    TURRENT APPLICANT: 2003-04-28
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; NUMBER OF SEQ ID NOS: 285684
; LENGTH: 3033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATGGGGTCAAAGTACTTGAAAGCTGCACAGGAGCTTCTGGATGAAGTTGTGAACGTGG
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US-09-938-842A-1337

US-10-225-066A-335

US-10-225-066A-335

US-10-225-066A-335

US-10-225-066A-335

US-10-424-599-7028

US-10-424-599-7028

US-10-437-963-31585

US-10-437-963-31586

US-10-437-963-31586

US-10-437-963-31586

US-10-437-963-31586

US-10-425-114-13359

US-10-425-114-13359

US-10-425-114-13359

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US-10-425-114-13349

US-10-425-114-13349

US-10-425-115-118580

US-10-425-114-13349

US-10-425-115-118580

US-10-225-066A-819

US-10-225-068-235

US-10-225-068-235

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      -10-424-599-130628
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Sequence 7804, Ap
Sequence 131558,
Sequence 63874, A
Sequence 141176,
Sequence 1337, Ap
                                                                                                                                                                                                         July 29, 2005, 08:10:18; Search time 1673 Seconds (without alignments) 10580.930 Million cell updates/sec
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'Cgn2_6/ptodata/1/pubpna/USO7 PUBCOMB.seq.*

'Cgn2_6/ptodata/1/pubpna/USO6 PUBCOMB.seq.*

'Cgn2_6/ptodata/1/pubpna/USO6 PUBCOMB.seq.*

'Cgn2_6/ptodata/1/pubpna/USO6 PUBCOMB.seq.*

'Cgn2_6/ptodata/1/pubpna/USO8 PUBCOMB.seq.*

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'Cgn2_6/ptodata/1/pubpna/USO9 PUBCOMB.seq.*
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Sequence 17, Appl Sequence 17, Appl Sequence 819, Appl Sequence 2481, Appl

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Sequence 2154, Ap Sequence 55280, A Sequence 905, App Sequence 905, App

Post-processing:

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Minimum DB Maximum DB

Scoring table:

Searched:

Title: Perfect score:

Sequence:

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Sequence 3524, Ap Sequence 118586, Sequence 10301, A Sequence 61918, A Sequence 237574, A Sequence 31974, A Sequence 5047, Ap Sequence 5047, Ap Sequence 118580, Sequence 118580, Sequence 118580, Sequence 118580, Sequence 2154, Ap Sequence 2154, Ap

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i Sequence 13353, Application US/10425114

i Publication No. US20040034888A1

i GENERAL INFORMATION:

i APPLICANT: Liu, Jingdong

i APPLICANT: Liu, Jingdong

i APPLICANT: Zhou, Yihua

i APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

i APPLICANT: Tabaska, Jack E

i APPLICANT: Application Steven E

i APPLICANT: Description Norder Acid Molecules and Other Molecules Associated With

ITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

ITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 39-21(53131)

CURRENT FILING DATE: 2003-04-28

i NUMBER OF SEQ ID NOS: 73128

i LENGTH: 1555
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                           GAAAAGGAATCTACAAAGAGGAGAAATTCTCAGAGAGCGTGAAAGCGAATAGGGAATCAA 980
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Sequence 7804, Application US/10425114

Sequence 7804, Application US/2040034888A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Applicant: Acvalic, David K.
APPLICANT: AppliCANT: Abaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Dants and Uses Thereof for Plant Improvement
TITLE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 7804
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                                                                                                                                                               Length 1555;
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; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: JC-GMST02400042B10_FLI
US-10-425-114-13353
                                                                                                                                                            Score 392; DB 18;
Pred. No. 7.4e-81;
0; Mismatches 129;
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Best Local Similarity 78.4%;
Matches 468; Conservative
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Alou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424, S99
CURRENT APPLICATION NUMBER: US/10/424
NUMBER OF SEQ ID NOS: 285684
ENGINE SEQ ID NOS: 285684
LENGTH: 1892
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US-10-424-599-63874
                                                                      Score 353; DB 18;
Pred. No. 1.1e-71;
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                                                                      12.9%;
72.6%;
                                                                   Query Match 12.9
Best Local Similarity 72.6
Matches 471; Conservative
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ORGANISM: Glycine
      US-10-424-599-133558
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Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Road Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Car Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 133558
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                                                                                                 Score 378.2; DB 18; Length Pred. No. 1.3e-77; 0; Mismatches 173; Indels
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OTHER INFORMATION: Clone ID: PAT_MRT3847_91608C.1
OTHER INFORMATION: Clone ID: 700684286_FLI
                                                                                                 Query Match
Best Local Similarity 73.64;
Matches 482; Conservative
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US-10-424-599-133558
          ; OTHER INFORMAT
US-10-425-114-7804
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: AND USEN THOMAS J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ. ID NOS: 285684
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                                                                                                       CTGCTCAAAGACAAGAACTTCAAATGAAAAAAGCCAAGCTTCTTGCCATGCTTGAAGAGG 1027
                                                                                                                                                         TGGAGCAAAGGTACAGACAGTACCATCACCAAATGCAAATAATTGTATTATCATTTGAGC 1087
                                                                                                                                                                                                            AGCAATTCAGATGCCTAAAGGATGCAATTGCTGAGCAAGTAAAGGCGACGAGCAAGAGTT 1207
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  Length 1892;
Score 352.6; DB 18; Length
Pred. No. 1.4e-71;
0; Mismatches 189; Indels
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US-10-424-599-141176
Query Match
Best Local Similarity 71.1%;
Matches 466; Conservative
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ORGANISM: Glycine max
FEATURE:
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APPLICANT: Kreps, Joeff
APPLICANT: Kreps, Joeff
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938, 842A
PRIOR APPLICATION NUMBER: US 60/227, 866
PRIOR APPLICATION NUMBER: US 60/227, 866
PRIOR APPLICATION NUMBER: US 60/264, 647
PRIOR PLING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-6
PRIOR FILING DATE: 2001-06-22
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      DB 18; Length 3311;
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   Score 346.8; DB 18;
Pred. No. 4.3e-70;
0; Mismatches 197;
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Query Match
Best Local Similarity 70.6%;
Matches 476; Conservative
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ORGANISM: Arabidopsis thaliana
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Best Local Similarity 65.2%;
Matches 534; Conservative
   Harper, Jeff
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larity 65.2%; Pred. No. 5.1e-65;
Conservative 0; Mismatches 264;
                                   ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1337
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1337
                                                                                  Query Match
Best Local Similarity
Matches 534; Conserv
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Sequence 1337, Application US/09938842A Publication No. US20040009476A9 GENERAL INFORMATION:

RESULT 8 US-09-938-842A-1337

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Pred. No. 5.1e-65;
0; Mismatches 264;
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APPLICANT: ADAM, LUC U
APPLICANT: HEARD, Jacqueline E
APPLICANT: HEARD, Jacqueline E
APPLICANT: PILGRIM, Marsha L
APPLICANT: JIANG, Cai-Zhong
APPLICANT: JIANG, Cai-Zhong
APPLICANT: JIANG, Cai-Zhong
APPLICANT: PILGRIM, Robert A
APPLICANT: PILGRIM, Robert A
APPLICANT: PINEMEN, Omaira
APPLICANT: PINEMEN, Comaira
APPLICANT: PINEMEN, Condaira
APPLICANT: PINEMEN, Condaira
APPLICANT: PROUN, Pierre E
TITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants
FILE REPERBNCE: MBI0036-2 US
CURRENT FILING DATE: 2002-08-09
FRIOR FILING DATE: 2001-04-18
FRIOR FILING DATE: 2001-04-18
FRIOR FILING DATE: 2001-08-09
FRIOR FILING DATE: 2001-12-05
FRIOR PRIOR PLICATION NUMBER: 60/336,049
FRIOR FILING DATE: 2001-12-11
FRIOR PLING DATE: 2001-12-11
FRIOR PLING DATE: 2001-12-11
FRIOR PLING DATE: 2001-12-11
FRIOR PLING DATE: 2001-12-11
FRIOR APPLICATION NUMBER: 10/171,468
FRIOR APPLICATION NUMBER: 10/171,468
FRIOR PLING DATE: 2001-12-11
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FRIOR FILING DATE: 2001-13-11
FRIOR APPLICATION NUMBER: 10/171,468
FRIOR FILING DATE: 2001-13-11
FRIOR APPLICATION NUMBER: 10/171,468
FRIOR FILING DATE: 2001-13-11
1109 GAGCTCTTCAACAACTGGGAATGATTCAACATCCTTCCAATAATGCTTGGAGACCTCAAC 1168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Mendel Biotechnology, Inc. APPLICANT: RATCLIFFE, Oliver APPLICANT: RIECHMANN, JOSE Luis APPLICANT: ADAM, Luc J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Arabidopsis thaliana
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US-10-225-066A-335
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Best Local S:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: A STRESS-RESPONSIVE PROMOTER AND A GENE CORDING FOR A STRESS-RESE
TITLE OF INVENTION: TRANSCRIPTION FACTOR
FILE REFERENCE: RFH14-0247
FILE REPERENCE: RFH14-0247
CURRENT APPLICATION NUMBER: US/10/495,918
CURRENT FILING DATE: 2004-05-18
PRIOR APPLICATION NUMBER: JP 2001-353038
PRIOR FILING DATE: 2002-01-39
PRIOR FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 166
SEQ ID NO S: 166
SEQ ID NO 153
LENGTH: 2043
                                                                   GCCAGGTGTCTAACTGGTTCATAAATGCTCGAGTTCGATTATGGAAGCCAATGGTAGAAG 1516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 11.9%; Score 324.6; DB 21; Length Best Local Similarity 65.2%; Pred. No. 5.1e-65; Matches 534; Conservative 0; Mismatches 264; Indels
                                                                                                                                                                                                    1517 AAATGTACTTGGAAGAGTGAAGAATCAAGAACAAAACA 1555
                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 153, Application US/10495918; Publication No. US20050009187A1; GENERAL INFORMATION: APPLICANT: RIKEN
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; LOCATION: (1)..(2040)
US-10-495-918-153
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Pred. No. 5.6e-65;
0; Mismatches 264; Indels
                  THE KEKEKENCE, MEL-OUG/ CIT.

CURRENT PELING DATE: 2003-02-25

FRIOR PELING DATE: 2003-02-25

FRIOR PELING DATE: 2003-02-25

FRIOR PELING DATE: 2001-04-18

PRIOR FILING DATE: 2001-08-09

PRIOR PILING DATE: 2001-08-09

PRIOR PELING DATE: 2001-08-09

PRIOR PELING DATE: 2001-08-09

PRIOR PELING DATE: 2001-08-22

PRIOR PELING DATE: 2001-11-19

PRIOR PILING DATE: 2002-06-14

PRIOR PILING DATE: 2002-06-14

PRIOR PILING DATE: 2002-08-09

PRIOR PILING DATE: 2002-08-09

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Best Local Similarity 65.2%;
Matches 534; Conservative
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US-10-374-780A-2671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 2671
LENGTH: 2385
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807 ATTCCGATGACATGAAGGCTAAATCCCAACTATTCTCATCGAAAAAGGGTAGTTGCGGAA 866
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                                                                                                                            367 ATGATAAACCTGTCGGAGAATCATCGGCCGCCTGGAGGAGAAGGTTCCGGTGGCGGAG 926
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                                                                            878 TGCCTTTGGCTAGTGATGTCAACACTAATAGTTCTGGTGGTGGAAAGTAGCAGCAGGC 937
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APPLICANT: Dubell III, Arnold T
APPLICANT: Pineda, Omaira
APPLICANT: Yu, Guo-Liang
IIILE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1517 AAATGTACTTGGAAGAAGTGAAGAATCAAGAACAAAACA 1555
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Publication No. US20040019927A1
GENERAL INFORMATION:
APPLICANT: Sherman, Bradley K
APPLICANT: Alechmann, Jose Luis
APPLICANT: Heard, Jacqueline E
APPLICANT: Heard, Jacqueline E
APPLICANT: Ratcliffe, Oliver
APPLICANT: Reuber, T. Lynne
APPLICANT: Reuber, T. Lynne
APPLICANT: Reddie, James
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Keddie, James
Broun, Pierre E
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Sequence 9882. Application US/10425114
; Sequence 9882. Application No. US20040034888A1
; GENERAL INFORMATION:
   APPLICANT: Liu, Jingdong
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua K.
   APPLICANT: Coreen, Steven E
; APPLICANT: Goreen, Steven E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313) B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 9882
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867 ATGATAAACCTGTCGGAGAATCATCGGCCGGCGCTGGAGGAGAAGGTTCCGGTGGCGGAG 926
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US-10-425-114-9882
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US-10-425-114-9882
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APPLICANT: TINEDA, Omaira
APPLICANT: YU, Guo-Liang
APPLICANT: YU, Guo-Liang
APPLICANT: YU, Guo-Liang
TITLE OF INVENTION: Pietre E
TITLE OF INVENTION: Yield-Related Polymucleotides and Polypeptides in Plants
FILE REFERENCE: MB10036-2 US
CURRENT FELICATION NUMBER: US/10/225,066A
CURRENT FILING DATE: 2002-08-09
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR PLICATION NUMBER: 60/338,692
PRIOR FILING DATE: 2001-12-01
PRIOR FILING DATE: 2001-12-11
PRIOR FILING DATE: 2001-13-11
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Pred. No. 5.6e-65;
0; Mismatches 264; Indels
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US-10-225-066A-335
i Sequence 335, Application US/10225066A
publication No. US20050160493A9
GENERAL INFORMATION:
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APPLICANT: RATCLIFFE, Oliver
APPLICANT: RIECHMANN, JOSE LUIS
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DUBELL, Arnold T
HEARD, Jacqueline E
PILGRIM, Marsha L
JIANG, Cai-Zhong
REUBER, T. Lynne
CREELMAN, Robert A
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ORGANISM: Arabidopsis thaliana
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Best Local Similarity 65.2%;
Matches 534; Conservative
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LENGTH: 2385
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US-10-437-963-41007
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; Publication No. US20040031072A1
; GENERAL INPORMATION:
; APPLICANT: La Rowalic David K
; APPLICANT: La Rowalic David K
; APPLICANT: Cao Yinua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: 103.23) B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 7028
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                                                                                                                                                                                                                         241 AGGAATGATTCAGCCCAATGCATGCATGGCCCCCAGAGAGGCTTGCCTGAACGAGCTGTTTC 300
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                                                                                                                  GCAAATTGTGGTATCATCATTTGAGCAAGCAGCGGGTTATGGGGGCGGCAAAATCTTACAC
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77.6%; Pred. No. 1.4e-62;
tive 0; Mismatches 110; Indels
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Best Local Similarity 77.6
Matches 380, Conservative
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                     1309 TAATGCAGCACCTGAGCTTTCCACTGCTGAGAGCAAGAGCTTCAGAACAAAATGGCAAA 1368
                                                                                 AATAATTGTATTATCATTTGAGCAAGTAGCAGGAATTGGATCAGCCAAATCATACACTCA 1124
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledoms; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 786)
Buell, C.R., Hart, A., Baker, B., Tanksley, S., Fry, W., Smart, C., Restrepo, S., Griffiths, H., van der Hoeven, R., Tesi, J. and Generation of a set of potato cDNA clones for microarray analyses Unpublished (2002)
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/organism="Solanum tuberosum"
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Compugen Ltd.
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Copyright (c) 1993 - 2005
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Solanum tuberosum (potato) Solanum tuberosum

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.

1 (bases 1 to 743)

S Buell,C.R., Hart,A., Baker,B., Tanksley,S., Fry,W., Smart,C., Restrepo,S., Griffiths,H., van der Hoeven,R., Tsai,J. and Karamycheva,S.A.

Generation of a set of potato cDNA clones for microarray analyses Unpublished (2002)

On Jun 10, 2002 this sequence version replaced gi:21369213.

Other ESTS: EST617758

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr. Rockville, MD 20850, USA

Email: potato-array@tipr.org

This clone can be obtained from the University of Arizona Genomics in the Contact of the Contact can be obtained from the University of Arizona Genomics in the University of Arizona Genomics
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/clone_lib="Generation of a set of potato cDNA clones for microarray analyses mixed potato cissues a mixed potato rissues for microarray analyses mixed potato cissues in the set of supplier: Combination of untreated and Phytophthora infestans created libraries of stclons, leaves, leaflets, axillary buds of stem explants, petioles, germinating eyes, tubers, or roots.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Solanum tuberosum"
/mol type="mRNA"
/cultivar="Kennebec or Binjte"
/db_xref="taxon:4113"
/clone="STWH158"
/tissue_type="mixed tissues"
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Location/Qualifiers
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamida; Solanales; Solanaceae; Solanum.

I (Dases 1 to 699)

Buell,C.R., Hart,A., Baker,B., Tanksley,S., Fry,W., Smart,C., Restrepo,S., Griffiths,H., van der Hoeven,R., Tsai,J. and Karamycheva,S.A.

Generation of a set of potato cDNA clones for microarray analyses Unpublished (2002)

On Apr 17, 2002 this sequence version replaced gi:20171732.

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA
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                       182 CATGGGAATAGTAATAATAATATTCAGACACTTTATTTGATGAACCCTAACAATAT
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                                                                                                                                                                          122 TACTATCAAGGAACCTCGGATAATACTAATATACAAGCTGATCATCAACAACATCATAAT
                                                                                                                                                                                                                               211 CATGGGAATAGTAATAATAATATTCAGACACTTTTATTTGATGAACCCTAACAATTAT
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/dev stage="12-14 weeks post harvest"
/lab_host="SOLR"
/clone lib="CSTR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK(-); Site_1 = 1: EcoRI; Site_2:
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: EcoR
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The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
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1 (bases 1 to 756)
van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Chiemingo, A., Generations of ESTs from sprouting potato eyes
Unpublished (2000)
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                                                                                               AACTICICAAAGCITAGAGAGCIACCACCCGAAGAIAGACAGIIAGITACA-----
                                                                                                                                                                                                                                                    Score 718.6; DB 4; Length 756;
Pred. No. 2e-158;
0; Mismatches 4; Indels 10;
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/cultivar="Kennebec"
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BG593861
BG593861.1 GI:13612001
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al Similarity 98.1%;
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                                                                                                                                                                  /tissue type="mixed tissues"
/lab_host="SOLR"
/lab_host="SOLR"
/clone_lib="mixed potato tissues"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; supplier: Combination of untreated and Phytophthora
infestanse treated libraries of stolons, leaves, leaflets,
axillary buds of stem explants, petioles, germinating
eyes, tubers, or roots."
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGAAGAAAGAATTTTTTTTGCAGATATGTACTATCAAGGAACCTCGGATAATACTAATA 181
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                                                                                                                                                                                                                                                                                                                                                                          AAAAATATAGATCAGTCTGACAAGAAGGCAACTTCTCAAAAGCTTAGAGAGCTACCACCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   482 ATCAATCTCAGCAGGTGATAGTACCATCGTCGACGGGGGTTTCTGCCACGTCATGTGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCGACAGCAGCAACAACAGCAAGCGGTCTATCTCTAAGCCTTTCTCCTCAGCTACAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  602 ACGACAGCAGCAACAACAACAAGGGGGTCTATCTCTAAGCCTTTCTCCTCAGCTACAAC
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                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                  24.4%; Score 666.4; DB 5; Length 699; 98.4%; Pred. No. 4.1e-146; ive 0; Mismatches 1; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        662 AGCAAATTAGTTTCAATAACAATATTTCATCCTCATCA 699
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                                                                                                              /mol_type="mRNA"
/cultivar="Kennebec or Binjte"
/db_xref="taxon:4113"
/clone="STMEMS4"
                                                                                                   /organism="Solanum tuberosum"
                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                              Matches 687; Conservative
                                                         primer: T3.
                                                                                                                                                                                                                                                                                                                                Similarity
                                                         Sed
                                                                                                                                                                                                                                                                                                                                                                          12
                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
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GATGCAATTGCTGAGCAAGTAAAGGCGACGAGCAAGAGTTTAGGTGAAGAGGAAGGCTTG 1227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAAAGAGCTGTCTCTGTCCTTCGTGCTTTGGGCTTTTCGAGCATTTTCTTCATCCTTACCCA 1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGGATTCAGACAAATCATGCTTGCTAAGCAAACGGGGCTAACAAGGAGCCAGGTGTCT 1467
                                     EST 18-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1108 GCCAAATCATACACTCAATTAGCTTTGCAAGTTTCGAAGCAATTCAGATGCCTAAAG 1167
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                                                                                                                                                                                                                                             Lycopersicon esculentum (tomato)
Lycopersicon esculentum
Lucypersicon esculentum
Eukaryora, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (Dases 1 to 685)
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T.,
Holt,J.E., Lianap,F., Upton,J., Craven,M.B., Bowman,C.L., Ahn,S.,
C.M., Fraser,C.M., Mattin,G.B., Tanksley,S.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="comato callus, TAMU"

/clone_lib="comato callus, TAMU"

/hote="Weetcor: pBlueScript SK(-); Site_l: EcoRl; Site_2:
Xhol; supplier: Glovannoni laboratory; clEC - Cotyledons
of seedlings 7-10 days post-germination were excised, cut
at both ends and placed on MS medium with no selection.

Mixed callus was harvested at 25 and 40 days and included
undifferentiated masses. Tomato Callus EST Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GATGCAATTAGTGAGCAAGTGAAGGCGACGAGGAAGAGTTTAGGTGAAGATGAAGGCTTG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 GGAGGGAAAATTGAAGGCTCAAGACTCAAATTTGTGGACCATCATCTAAGGCAACAACGC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09
685 bp mRNA linear EST 18-MAY-20
EST278301 tomato callus, TAMU Lycopersicon esculentum cDNA clone
CLEC33H16, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 GCGCTGCAACAGCTAGGAATGATGCTAGAATGCTTGGAGACCCCAAAGAGGTTTACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: CUGI
Clemson University
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 23.3%; Score 638.6; DB 2; Length 685; Best Local Similarity 96.4%; Pred. No. 1.5e-139; Matches 666; Conservative 0; Mismatches 19; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Giovannoni,J.
Generation of ESTs from tomato callus tissue
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissue type="callus"
/dev stage="25-40 days old"
/lab_host="XL1-Blue MRF'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:4081"
/clone="cLEC33H16"
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                                                                                                                                                                              AW034617.1 GI:5893373
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727 bp mRNA linear EST 07-MAR-2003 Solanum tuberosum cDNA clone cSTE1A17 5' sequence,
(Plant Journal, 1996). Small microtubers develop from axillary buds atteached to stem explants when placed on a high sucrose medium (10%). Visible morphological changes occur synchronously at day five in the axillary buds. The first library, GSTA (1-20) consists of axillary buds harvested on days 1-3. This targets those genes involved in induction of the microtubers. The following libraries, CSTA (1-40) and CSTA (1-60), capture genes involved in tuber initiation and outgrowth. This library is noted as P3 in Tankeley lab notebooks.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTAAGCCTTTCTCCTCAGCTACAACAGCAAATTAGTTTCAATAACAATATTTCATCCTCA 696
                                                                                                                                                                                                                                                                                                                                                                                                                                             GGAACCTCGGATAA---TAATATACAAGCTGATCATCAACAACAACATCATAATCATGGGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               479 GGGGTTTCTGCCACGTCATGTGGCGGGATTACCACGGACTTGGCGTCTCAATTGGCGTTTT
                                                                                                                                                                                                                                                                                                                                        GGAACCTCGGATAATACTAATACAAGCTGATCATCAACAACGTCATAATCATGGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 517 GGGGTTTCTGCCACGTCATGTGGCGGGATCACCACGGACTTGGCGTCTCAATTGGCGTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGAGGCCGATTGTGGTGGGAACACCGACAGCAGCAGCAACAACAGCAAGGCGGTCTATCT
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                                                                                                                                                                                                                                                      Length 708;
                                                                                                                                                                                                                                                      Score 608; DB 4; Length 70
Pred. No. 2.5e-132;
0; Mismatches 25; Indels
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                                                                                                                                                                                                                                                   Query Match 22.2%;
Best Local Similarity 94.2%;
Matches 669; Conservative
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EST517371 CSTE S
mRNA Sequence.
BI176426
BI176426.1 GI:1
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BI176426
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1 (bases 1 to 708)

2 van der Hoeven, R., Bezzerides, J., Bachem, C., Visser, R., Karamycheva, S.A., Tsai, J., Van Aken, S., Utterback, T., Chiemingo, A., Bougri, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B. Generation of ESTs from in vitro grown microtubers (2001b)

Unpublished (2001)

Contact: Robin Buell

The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@tigr.org

This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL:

http://genome.arizona.edu/orders/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B1920940 708 bp mRNA linear EST 10-MAR-2003 EST540875 potato microtubers, in vitro-grown Solanum tuberosum cDNA clone cSTE26N18 5' end, mRNA sequence. B1920940 GI:16216968
                                                                                                                                                                                                                                                                                                                                                                          GAAGAAGTGAAGAATCAAGAACAAAAACAGTACTAATACTTCAGGAGATAACAAAACAAA 1587
                                                                                                                                                                                                          GAGACCAATATAAGTGCTCCAAATGAAGAGAAACATCCAATTATTACTAGCAGCTTATTA 1647
                                                                                                                                                                                                                                                                                             CAAGATGGTATTACTACTACTCAAGCAGAAATTTCTACCTCAACTATTTCAACTTCCCCT 1707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lbe_motato microtubers, in vitro-grown"
/note="Vector: pBluescript SK(-); Site 1: EcoR1; Site 2:
Xhoī; Tissue supplied by Christian Bachem and Richard
Visser (Department of Plant Breeding, Wageningen
University, The Netherlands); sequencing by The Institute
for Genomic Research. The cSTA libraries will attempt to
capture the induction and initiation/initial growth of the
tuber in an in vitro system as described in Bachem et al.
                                                                GAAGAAGTGAAGAATCAAGAACAGTAGTAATACTTCAGGAGATAACAAAAACAAA 480
    AAAGACTCAGACAAAATCATGCTTGCTAAGCAAACGGGGCTAACAAGGAGCCAGGTCTCT 360
                                                                                                                                                                                                                                    CAAGATGG-----TACTACTCAAGCAGAAATTTCTACCTCAACTATTTCAACTTCCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                stem explants; growing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue type="axillary buds of sink-tubers"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GATAATACTACTACTACTGTTGATCATATTG 1798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Solanum tuberosum"
/mol type="mRNA"
/cultivar="Bintje"
/db_xref="taxon:4113"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="7, 8 and 10 days"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGAATACTACTACTGTTGATCATATTG 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Solanum tuberosum (potato)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Solanum tuberosum
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                                           1468
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  301
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AUTHORS
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238 336 298 396 358 456 418

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Lycopersicon esculentum (tomato)
Lycopersicon esculentum
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.

1 (bases I to 644)
Alcala, Virebalov, J. White, R., Matern, A.L., Holt, I.E., Liang, F., Upton, J., Hansen, T., Craven, M.B., Bowman, C.L., Ahn, S.,
Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AW930221 644 bp mRNA linear EST 18-MAY-2001 EST340678 tomato fruit mature green, TAMU Lycopersicon esculentum cDNA clone cLEF41L1 5', mRNA sequence.

AW930221.1 GI:8105622
                               298 CAGCAGCAGTTACTTTCCTGAATTCTTCACCAGGAAGCAACGCAGCATTGCCATGCG 357
                                                                                                             423
                                                                                                                                       358 AATATACAACACGCGCGCTGCAACAGCACTTTGTCGGTGTGCCTCTTCCGGCAGTA 417
                                                                                                                                                                                                                          483
                                                                                                                                                                                                                                                    543
                                                                                                                                                                                                                                                                                                                                                                  478 CAAICTCAGCAGGTGATAGTACCATCGTCGACGGGGGTTTCTCTCCCCACGTCATGTGGGCGGG 537
                                                                                                                                                                                                                                                                                                                                                                                                                                             544 ATCACCACGGAC-TTGGCGTCTCAATTGGCGTTTCAGAGG-CCGATTCCGACACCACAAC 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              657 AGCAAATTAGTTT-AATAACAATATTTCAGCCTCATCACCAAGGACAAATAATGTTACTA 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          602 ACCGACAGCAGCAACAACAGCAAGGCGGTCTATCTCTAAGCCTTTCTCCTCAGCTACAAC 661
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/dev_etage="mature green (3-5 days pre-ripening)"
/lab_host="sOLR"
/clone_lib="tomato fruit mature green, TAMU"
/clone_lib="tomato fruit mature green, TAMU"
/clone_lib="tomato fruit wature green, TAMU"
/clone_lib="tomato fruit wature green, TAMU"
/hote="Yoctor: pBlueScript SK(-); Ste 1: BcoR1; Site 2:
/hot clbF - Fruit ware tagged at the lom stage and
harvested 3-5 days prior to ripening. Fruit were cut in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               538 ATTACCACGGACTTTGGCGTCTCAATTGGCGTTTCAGAGGCCCCGATTGTGGTGTCGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  662 AGCAAATTAGTTTCAATAACAATATTTCATCCTCATCACCCAAGGACAAATAATGTTACTA
                                                                                                                                                                                                                       AGTITGCACGATCAGATCATCATCATGGACTTTTACAGCGCATGTGGAACAACAAGAT
                                                                                                                                                                                                                                                                                                                                     CAATCTCAGCAGGTGATAGTACCATCGTCGACGGGGGTTTCTGCCACGTCATGTGGCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             598 ACCGACAGCAACAACAACAACGAAGGCGGTCTATCTCTAAGCCTTTCTCCTCAGCAACAAC
                                                                                                             364 AATATACAACACGCCCCCCTGCAACAGCACTTTGTCGGTGTGCCTCTTCCGGCAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Lycopersicon esculentum"
/mol type="mRNA"
/cultivar="TA496"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Generation of ESTs from tomato fruit tissue Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:4081"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prime sequence.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  722 TTAGGGGAACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: CUGI
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//done_lbb="cSTE"
//done_lbb="cSTE"
//done_lbb="cSTE"
//done_lbb="cSTE"
//done_Tbb="cSTE"
//done="Vector: pBluescript SK(-); Site_1: EccRI; Site_2: XhoI; Tissue supplied by Christian Bachem and Richard
Visser (Department of Plant Breeding, Wageningen
University, The Netherlands). The cSTA libraries will
attempt to capture the induction and initiation/initial
growth of the tuber in an in vitro system as described
Bachem et al. (Plant Journal, 1996). Small microtubers
develop from axillary buds attached to stem explants when
placed on a high sucrose medium (10%). Visible
morphological changes occur synchronously at day five in
the axillary buds. The first library. CSTA (1-20) consists
of axillary buds harvested on days 1-3. This targets
those genes involved in induction of the microtubers. The
following libraries, CSTA (21-40) and CSTA (1-60),
capture genes involved in tuber initiation and outgrowth.
This library is noted as P3 in Tanksley lab notebooks."
                                                                                                                                                                                                                                                                      Unpublished (2001)
Contact: Robin Buell
Contact: Robin Buell
First Inture for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850, USA
Email: potato-array@tigr.org
First clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
Seq primer: M13F-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        187 GCTGATCATCAACAACGTCATAATCATGGGAATAGTAATAATAATAATATTCAGACACTT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATTTGATGAACCCTAACAATTATATGCAAGGCTACACTACTTCTGACACA---CAGCAG 303
                                                Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnollophyta, eudicotyledons, core eudicots, asterids, lamidas, Solanales, Solanaceae, Solanum.

(bases 1 to 727)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127 GAAAGAATTTTTTTTGCAGATAIGTACTATCAAGGAACCTCGGATAATACTAATATACAA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GAAAGAATTTTTTTTGCAGATATGTACTATCAAGGAACCTCGGATAA---TAATATACAA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96
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                                                                                                                                                              van der Hoeven,R., Bezzerides,J., Bachem,C., Visser,R., Cho,J., Chiemingo,A., Bougri,O., Buell,C.R., Ronning,C., Tanksley,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TATAGATCAGTCTGACAAGAAGGAACTTCTCAAAGTTTAGAGAGCTACCACCGGAAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 GCTGATCATCAACATCATAATCATGGGAATAGTAATAATAATAATATTCAGACACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 TATAGATCAGTCTGACAAGAAGGCAACTTCTCAAAGCTTAGAGAGCTACCACCCGAAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db xref="taxon:4113"
/clone="cSTE1A17"
/tissue_type="axillary buds of stem explants; growing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                               Generation of ESTs from in vitro grown microtubers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Bintje"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="7, 8 and 10 days"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
  Solanum tuberosum (potato)
                                                                                                                                                                                                                          Baker, B.
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                         ORGANISM
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1557 TACTAATACTTCAGGAGATAACAAAAACAAAGAGACCAATATAAGTGCTCCAAATGAAGA 1616
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                                                                                                                                                                                                                                                                                                                                                                                                                1497 ATGGAAGCCAATGGTAGAAGAAATGTACTTGGAAGAAGTGAAGAATCAAGAACAAAAACAG 1556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1737 CAATTICICCTICCTIGGTICATICAACAIGGATAATACTACTACTACTIGATCATAT 1796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGAAAACAACGCGAAAAAGCAAAGAA---ATGACATGCCACAAGTTTTCTCCAAGTAGTAT 1853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTTTCATCTGTTGACATGGAAGCCAAAGCTAGAGAATCATCAAATAAAGGGTTTACTAA 1913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1914 TCCTTTAATGGCAGCATACGCGATGGGAGATTTTGGAAGGTTTGATCCTCATGATCAACA 1973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST 10-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 GAAACAACCAATTATTACTAGCAGCTTATTACAAGATGG-----TACTACTCAAGCAGA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 AATTTCTACCTCAACTATTCAACTTCCCCTACTGCAGGTGCTTCACTTCATCATGCTCA 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="tomato shoot/meristem"
/note="Vector: pBluescript SK(-); Site_l: EcoRl; Site_2:
Xhol; Small expanding leaves from the growing tip were
taken from greenhouse plants (4-6wks old TA496). Tissue
was immediately frozen in liquid nitrogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 TAGTAATACTTCAGGAGATAACAAAAACAAAGAGACGAATATAAGTGCTCCAAATGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1974 AATGACCGCGAATTTTCATGGAAATAATGGTGTCTCTTTACTTTAGGACTTCCTCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          476 AATGACCGCGAATTTTCATGGAAATAATGGTGTATCTCTTACTTTAGGACTTCCTACTTC
                                                                                   /organism="Lycopersicon esculentum"
/mol type="mRNA"
/mol type="mRNA"
/culfivar="TA496"
/db xref="taxon:4081"
/clone="cTOP23N12"
/dev stage="developing shoots from 4-6wks old plants"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAACATCCAATTATTACTAGCAGCTTATTACAAGATGGTATTACTACTACTCAAGCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                              Length 630;
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                                                                                                                                                                                                                                                                                                                                              Query Match 20.7%; Score 565; DB 4; I
Best Local Similarity 95.4%; Pred. No. 3.4e-122;
Matches 606; Conservative 0; Mismatches 20;
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EST474950 tomato shoot/meristem Lycopersicon esculentum cDNA clone
cTOF23N12 5' sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGACCAATATAAGTGCTCCAAATGAAGAAAACTCCAATTATTACTAGCAGCTTATTAC 1648
|||| |||||||||||||||||||||
AGACGAATATAAGTGCTCCAAATGAAGAGAAACAACAATTATTACTAGCAGCTTATTAC 420
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Lycopersicon esculentum
Lycopersicon esculentum
Lycopersicon esculentum
Lycopersicon esculentum
Lycopersicon esculentum
Spermatophyta; Viidiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
Lybases 1 to 630)
Van der Hoeven, B. Bezzerides, J., Sun, H., Cho, J., Utterback, T.,
Hansen, C., Ronning, C. and Tanksley, S.
Generation of ESTs from tomato shoot/meristem tissue
Unpublished (2001)
                                                                                                                                                                                                                                  CGCTGCAACAGCTAGGAATGATGATGCAACCAAATGCTTGGAGACCCCCAAAGAGGTTTACCTG 120
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   'immature' and the
 half to verify the seeds were indeed 'immature' and the seeds and locules were discarded prior to freezing the pericarp"
                                                                                                                                                                 GAGGGAAAATTGAAGGCTCAAGACTCAAATTTGTGGACCATCATCTAAGGCAACAACAACGCG
                                                                                                                                                                                                                                                                                                                                                                  ACTGGTTCATTAATGCTCGAGTTCGATTATGGAAGCCAATGGTTGAAGAAATGTTAGCTTGG
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                                                                                Score 581.6; DB 2; Length
Pred. No. 4.2e-126;
0; Mismatches 19; Indels
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BG129304.1 GI:12629492
                                                                                 Query Match 21.3%;
Best Local Similarity 95.7%;
Matches 622; Conservative
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Capsicum annuum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Capsicum
1 (bases 1 to 610)
S Song, W.Y., Jeon, W.B., Kim, K.S., Lee, H.H., Ko, M.K., Kim, Y.S.,
Hong, J.C. and Oh, B.J.
Generation of Hot Pepper (Capsicum annuum) ESTs (Express Sequence
Tags) from Red Ripe Fruit (Song, et al.)
Unpublished (2004)
Contact: Boung-Jun Oh
Jeonnam Biotechnology Research Center
Namyang Bld. #603, 10-4 Gwangsan-dong, Dong-gu, Gwangju 501-180,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST 16-AUG-2004
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401 TIATATGCAAGGCTACACTACTTCTGACACAGCAGCAGCAGCAGTACTTTTCCTGAA 460
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                                                                                                                                                                                                                                                                                              581 İCATGGACTITIACAGCGCATGTGGAACAACCAAGATCAATCTCAGCAGGTGATAGTAGC
                                                    TTCTTCACCAGCAGCAAGCAACGCGCTTTGCCATGCGAATATACAACACGCGCCGCTGCA
                                                                              TCATGGACTITIACAGCGCATGTGGAACAACCAAGATCAATCTCAGCAGGTGATAGTACC
                                                                                                                                                                                                                                                                                                                                                           ATCGTCGACGGGGTTTCTGCCACGTCATGTGGCGGGATCACCACGGACTTGGCGTCTCA
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ВJ02039F01 ВJ02 Capsicum annuum cDNA 5', mRNA sequence.
CO909070
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19.4%; Score 531; DB 7; Length 61
Best Local Similarity 92.5%; Pred. No. 3.6e-114;
Matches 558; Conservative 0; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:4072"
/tissue type="red pepper fruit pericarp"
/clone lib="BJ02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Capsicum annuum"
/mol_type="mRNA"
/cultivar="Nokkwang"
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Fax: 82 62 607 6205
Email: bjo@biohub.re.kr
Plate: 039 row: F column: 01.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /done liberary force microtubers, in vitro-grown"
//done liberary force microtubers, in vitro-grown"
//note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
Xhol; Tissue supplied by Christian Bachem and Richard
Visser (Department of Plant Breeding, Wageningen
University, The Netherlands); sequencing by The Institute
for Genomic Research. The cSTA libraries will attempt to
capture the induction and initiation/initial growth of the
tuber in an in vitro system as described in Bachem et al.
(Plant Journal, 1996). Small microtubers develop from
axillary buds attached to stem explants when placed on a
high sucrose medium (10%). Visible morphological changes
occur synchronously at day five in the axillary buds
first library, cSTA (1-20) consists of axillary buds
harvested on days 1-3. This targets those genes involved
in induction of the microtubers. The following libraries,
cSTA (21-40) and cSTA (41-60), capture genes involved in
tuber initiation and outgrowth. This library is noted as
                                                                                                                                                                   Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Eukaryota; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids, Solanales; Solanaceae; Solanum.

1 (Dases 1 to 789)

2 (Dases 1 to 789)

3 van der Hoeven,R., Bezzerides,J., Bachem,C., Visser,R., Karamycheva,S.A., Tsai,J., Van Aken,S., Utterback,T., Chiemingo,A., Raramycheva,S.A., Tsai,J., Van Aken,S., Utterback,T., Chiemingo,A., Generation of ESTS from in vitro grown microtubers (2001b)

4 Unpublished (2001)

5 Contact: Robin Buell

The Institute for Genomic Research

7712 Medical Center Dr, Rockville, MD 20850, USA

Email: pocato-arrayeligr.org

This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL:
EST540943 potato microtubers, in vitro-grown Solanum tuberosum cDNA
clone cSTE27121 5' end, mRNA sequence.
B1921008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         207 TAATCATGGGAATAGTAATAATAATAATATTCAGACACTTTATTTGATGAACCCTAACAA 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .78
/ organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivaf="bintje"
/db_xref="taxon:4113"
/clone="cSTE27121"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue type="axillary buds of sink-tubers"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P3 in Tanksley lab notebooks.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="7, 8 and 10 days" /lab_host="SOLR"
                                                                                                                           Solanum tuberosum (potato)
Solanum tuberosum
                                                                         BI921008.1 GI:16217036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seg primer: T3.
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BE435130 721 bp mRNA linear EST 18-MAY-2001 EST406208 tomato breaker fruit, TIGR Lycoperaicon esculentum cDNA clone cLEG25M5, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAGCCAGGTGTCTAACTGGTTCATAAATGCTCGAGTTCGATTATGGAAGCCAATGGTAG 1513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCAGATGCCTAAAGGATGCAATTAGTGAGCAAGTGAAGGCGACGAGGAAGAGTTTAGGTG 120
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                         in Rio Grande x Money Maker)"
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Lycopersicon esculentum
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
asterids, lamids, Solanales, Solanaceae, Solanum, Lycopersicon.
1 (bases 1 to 721)
                                                                                                                                /clone lib="tomato resistant, Cornell"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xhol; cLER - Tomato Pseudomonas Resistant EST Library.
Directionally cloned cDNAs inserted into pBlueScript
SK(-) at 5' end with EcoR1 and 3' end with Xhol site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 GGAGCCAGGTCTCTAACTGGTTCATTAATGCTCGAGTTCGATTATAGGAAGCCAATGGTTG
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                                                                                                                                                                                                                                                                                                                                                               1214 AAGAGGAAGGCTTGGGAGGGAAAATCGAAGGCTCAAGACTCAAATTTGTGGACCATCATC
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                                                                                                                                                                                                                                                                18.9%; Score 517.8; DB 1; Length 553; llarity 96.0%; Pred. No. 4.6e-111; Conservative 0; Mismatches 22; Indels 0
   /mol type="mRNA"
/culcivar=%11.12 (358::Pto ir
/db xref="taxon:4081"
/clone="cLER5L8"
/tissuue_type="leaf"
/dev stage="14-week old"
/lab_hogt="SOLR"
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Matches 531; Conserv
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BE435130/c
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                                                                                                                              AATTCAGATGCCTAAAGGATGCAATTGCTGAGCAAGTAAAGGCGACGAGCAAGAGTTTAG 1210
                                                                                                                                                                                                                                                                                                                                                         GTGAAGAGGAAGGCTTGGGAAGAGAAATCGAAGGCTCAAGACTCAAATTTGTGGACCATC 1270
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Lycopersion esculentum (Company)

Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon. 1 (Daaes 1 to 553)

Nascenzo,M., He,X., Lyman,J., Matern,A.L., Vision,T., Holt,I.E., Liang,F., Upton,J., Roming,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Tanksley,S.D., Glovannoni,J.J., and Martin,G.B.

Generation of ESTs from Pseudomonas resistant tomato
                                                                               GTGAAGGGAAGGCATAGGAGGGAAAATTGAAGGGTCGAGACTCAAATTTGTAGACCATC 367
                       67
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BST244353 tomato resistant, Cornell Lycopersicon esculentum cDNA
Clone CLER5L8, mRNA sequence.
A1773253
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
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1213

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1273

180

1333

240

1393

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/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="PoABE14"
                                                                                                                                                                                                                                                                                                                                                                                                                                Solanum tuberosum (potato)
Solanum tuberosum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2251 AAAGGAAGTTAGGAATACTCTTATATTGTGTGAGGCCTTCTGGCCCAAGTCGGAGGACCC 2310
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Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E.,
Lang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,
Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and
Tanksley,S.D.
                                                                                                                                                                                                                                                                                                                                                                                                                            /clone lib="tomato breaker fruit, TIGR"
/note="Vector: pBluescriptSKmCUadapt; Site_1: EcoR1;
Site_2: XhoI; Fruit were harvested at the breaker stage
(first sign of lycopene accumulation on the blossom end
the fruit). Fruit were cut in half and the seeds and
locules were discarded prior to freezing the pericarp."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                  Generation of ESTs from tomato fruit tissue, breaker stage Unpublished (2000)
Contact: CUGI
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence
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                                                                                                                                                                                                                                                                       /organism="Lycopersicon esculentum"
/mol type="mRNA"
/cultivar="TA496"
                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:4081"
/clone="cLEG25M5"
                                                                                                                                                                                                                                   Location/Qualifiers
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/closue="Powder"abjoic stress treated leaf and root tissue"
/lab host="abjoic stress treated leaf and root tissue"
/lab host="bulloB-TonA"
/clone=lb="popeato abjoic; stress cDNA library"
/note="vector: pCWNSport6.1; Site 1: EcoRi; Site 2: Not!;
supplier: Solanum tuberosum var. Kennebec plants were
grown from cuttings on a 16hr light/θ hr dark cycle at 25
C for 3-4 weeks. Abjoic stress conditions were applied to
four separate sets of plants. Set 1 involved saturation of
the soil with 150 mM NaCl and tissues were harvested at
following application of the salt stress (leaves: 2hr,
6hr, 12hr, 1d, 2d, and 4d; roots:2hr, 6hr, 12hr, and 2d).
Set 2 were grown under the standard conditions and then
were water stressed by withdrawal of further watering
applications. Drought stressed plants were harvested after
cessation of watering (leaves: 3d, 3d, and 3d, rootes:3d
and 5d). Set 3 were grown under the standard conditions
and then were cold stressed by placement at 4 C. Cold
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d and heat-stressed roots were harvested at 6 hr,
12 hr, 1 d, and 4d. RNA was isolated from all tissues and
equal RNA from each tissue and stress was pooled to
construct the cDNA library. RNA sample." CK262102

BST708180 potato abiotic stress cDNA library Solanum tuberosum cDNA clone POABE14 5' end, mRNA sequence. CTAAATTATGTTTCCATTGCTTGTAATTGCAATTTTAATTTGAATTTTGTGCTATCATTAT 2708 Eukaryocta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum.

El (bases 1 to 96 March, Zismann, V., Karamycheva, S.A. and Baker, B. Generation of ESTs from abiotic stressed potato tissue
Lumpublished (2003)
Other ESTs: EST708181
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG. Tracheophyta; 91 90 CTAAAJTATGTTTCCATTGCTTGTAATTGCAATTTTATTTGAATTTTGTGCTATCATTAT 31 150 TGATATTTGTTACTCTCAATTTTGCATATAATTTGAAATATTTTTTGTACCTACTAGTTGT

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EST411755 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA
               lone cLEG28B4, mRNA sequence
                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1. .495
                           BE460264.1 GI:9504638
                                                                                                                                                                                                                                                                                                prime sequence.
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            Length 964;
            Score 476; DB 7; Length 96. Pred. No. 3.8e-101; 0; Mismatches 220; Indels
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             17.4%;
            Query Match
Best Local Similarity 72.6
Matches 687; Conservative
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                                       Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; asterids; Jamilds; Solanales; Solanaceae; Solanum; Lycopersicon. 1 (bases 1 to 495)
Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E., Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M., Mierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.
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                                                                                                                                                                                                                                                                             Generation of ESTs from tomato fruit tissue, breaker stage Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                           Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
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Best Local Similarity 96.6%; Pred. No. 2.9e-99;
Matches 478; Conservative 0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Lycopersicon esculentum"
/mol type="mRNA"
/cultivar="TA496"
/db zref="taxon:4081"
/clone="cLEG28B4"
/tissue type="Pericarp"
/dev stage="breaker"
/lab host="SOLR"
/clone lib="tomato breaker fruit, TIG
                                                                                                                                                                                                                                                                                                                                                                                  Clemson University Genomics Institute
Lycopersicon esculentum (tomato) Lycopersicon esculentum
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1522 TACTTGGAAGAGTG 1536 ||||||||||||||| 481 TACTTGGAAGAAGTG 495

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Search completed: July 29, 2005, 14:13:05 Job time: 8595 secs

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2 (bases 1 to 2735)
Chen, H., Rosin, F.M. and Hannapel, D.J.
A KNOX protein of potato interacts with several members of the TALE
family of transcription factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AP406697 2735 bp mRNA linear PLN 14-JUL-2003
Solanum tuberosum BEL1-related homeotic protein 5 (Bel5) mRNA,
complete cds.
AP406697
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1 (bases 1 to 2735)
Chen, H., Rosin, F.M., Prat, S. and Hannapel, D.J.
Chen, H., Rosin, F.M., Prat, S. and Hannapel, D.J.
Enteracting transcription factors from the three-amino acid loop extension superclass regulate tuber formation
Plant Physiol. 132 (3), 1391-1404 (2003)
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Direct Submission
Submitted (07-AUG-2001) Department of Horticulture, Iowa State
                                AY072175

AY099854

AY098854

AF153094

AK120813

AK120813

AK120813

AK070465

AK070465

AK06703

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AK06703

AK06899

AK121356

AK070563

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an, H., Rosin, F.M. and Hannapel, D.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
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CNS08CAM
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ORGANISM
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REFERENCE
AUTHORS
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TITLE
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  O
                                                                                                                                                                                                                                                                                                                                                                        Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q-|Cgn2_1/USPTO_epool/US10624201/runat_27072005_122957_10905/app_query.fasta_1.839
-Q-|Cgn2_1/USPTO_epool/US10624201/runat_27072005_122957_10905/app_query.fasta_1.839
-Q-|Cgn2_1/USPTO_epool/US10624201_runat_27072005_122957_10905/app_query.fasta_1.839
-UNITS=bite -START=1 -END--1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST-45
-UNITS=bite -START=1 -END--1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST-45
-UNITS=bite -START=1 -END-1 -TRANS=100 -TRANS=100000000
-UNITS=bite -START=1 -NORM=ext -HEAPSIZE=50 -MINLEN-0 -MAXLEN=2000000000
-USFR=US10624201_@CGN 1 1 5081 @runat_27072005_122957_10905 -NCPU=6 -ICPU=3
-NO MAAAP -LIARGEQUERS -NEG SCORRES=0 -WAIT -DSPEDCCK=100 -LONGLOG
-FGAPOP=10 -YGAPOP=10 -YGAPDXT=0.5 -DELOP=6 -DELEXT=7
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Solanum t
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AF375966 Lycopersi
                                                                            July 29, 2005, 11:50:07; Search time 8001 Seconds (without alignments) 4166.628 Million cell updates/sec
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                                                                                                                            US-10-624-201A-2
3563
1 MYYQGTSDNTNIQADHQQRH......GNKRFPTQLLPDFVTGNLGT 688
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             GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                                                         nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                   of hits satisfying chosen parameters:
                                                                                                                                                                                                                                              4708233 segs, 24227607955 residues
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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                                                                                                                                  GTTAATATTGTTGGAAAAAGCATCAAAGGAGATGATCAAAAAGAAGGATAATTCAATGAAT
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                                                  TyrHisHisGlnMetGlnIleIleValLeuSerPheGluGlnValAlaGlyIleGlySer
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YTTSDTQQQQLLFLNSSPAASNALCHANIQHAPLQQQHFVGYPLPAVSLHDQINHHG
LLQRWMNDQDSQQVIYPSSTTGVSATSCGGITTDLAGQCLAPQRF PTPQHRGQQQQQG
GLSLSLSPQLQQQISFNNNISSSSPRTNNYITRGTLDGSSSNWVLGSKYLKAAQELLD
GVNIVGKSIKGDDQKXDNSNNKESNPLASDVNTNSSGGGESSSRQKNEVAPUELTTAQ
RQELQMKKAKLLAMLEEVPGRYRQYHQMQIIVLSFEQVAGTGSAKSYTQLALHAISK
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SSILSSVDMRAKARESSNKGFTNPLMAAYAMGDFGRFDPHDQQMTANFGNNGYSLTL
GLPPSENLAMPVSQQNYLSNDLGSRSEMGSHVRMGYENDIDFCY
TGNLGT"
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protein_id="AAN03621.1"
db_xref="GI:22652115"
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                                                           /db_xref="taxon:4113"
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y, 257 Horticulture
Location/Qualifiers
                                       /mol_type="mRNA"
/cultivar="Desiree"
                                                                              /gene="Bel5"
148. .2214
/gene="Bel5"
/note="StBel5"
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ALQQLGMAQPNAWRPQRGLPERAVSVLRAWLFEHFLHPYPKDSDKIMLAKQTGLTRSQ
VSNWFINARVRLWKPMVEEMYLEEVKNQEQNSSNTSGDNKNKETNISAPNEEKQPIIT
SSLLQDGTTQAEISTSTSTSTSPTAALHHAINFSFLGSFNWENTTTYVDHIENNAKK
PRHDMHKFPSPSILSSVEMEAKARESTNKGFTNPLMAAYAMGDFGRPDPHQQMTAN
FHGNNGVSLTLGLPPENLAMPVSQQNYLSNELGSRPPEIGSHYNRMGYENIDFQSGNK
RFPTQLLPDFVTGNLGT"
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El (Dases 1 to 2636)
S Ron, N., Parnis, A. and Lifschitz, E. Direct Submission
L. Submission
L. Submitted (03-MAY-2001) Biology, Technion, Haifa, Israel
Location/Qualifiers
1. 2636
| Organism="Lycopersicon esculentum" | Mol Lype="mRNA" | Mol Lype="mRNA" | Mol Lype="mRNA" | Location | 
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/gene="BL2"
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1531 GTTCGATTATGGAAGG 468 G1 nAsnSerThrAshT 1591 CAAAACAGTAGTAATA 1651 AATGAAGACAACAAC 508 G1 nAlaGlut	SOURCE Solanum tuberosum (potato) ORGANISM Solanum tuberosum (potato) ORGANISM Solanum tuberosum Solanum tuberosum Solanum tuberosum Solanum tuberosum Solanum tuberosum Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum. REFERENCE 1 (bases 1 to 1898) AUTHORS Chen,H., Rosin,F.M., Prat,S. and Hannapel,D.J. TITLE Interacting transcription factors from the three-amino acid loop aversation superclass regulate tuber formation JOURNAL Plant Physiol. 132 (3), 1391-1404 (2003) PUBMED 12857821 REFERENCE 2 (bases 1 to 1898) AUTHORS Chen,H., Rosin,F.M. and Hannapel,D.J. TITLE A KNOX protein of potato interacts with several members of the TALE
93 SerLeutisAspGlnIIsAspGlnIIsAspGlnIIsAspGlnIIsAspGlnIII	388 MetGlnProAsnalaTrpArgProGlnArgGlyLeuProGluArgAlaValSerValLeu 407

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93
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Ames, IA 50011-1100, USA
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CGTGAAATTTCAACAACAATCATCAAGTTGGAATACTATCATCATCACATTACCATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----ArgThrAsnAsnValThrIleArgGlyThrLeuAspGlySerSerSer---
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319
56
100
86
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Conservative:
Mismatches:
Indels:
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Chen, H., Rosin, F.M. and Hannapel, D.J.
Direct Submission
Submitted (07-AUG-2001) Department of
University, 257 Horticulture Hall, An
Location/Qualifiers
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66.84%
56.86%
37.38%
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3 (bases 1 to 1898)
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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               JOURNAL
REFERENCE
AUTHORS
                                                             TITLE
JOURNAL
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	173 GINILeSerPhasnaban	258 GlyGluSerSerArgGlnLygAsnGluValAlaValGluLeuThrThrAlaGlnArg 277	CAAGAAATACAGATGAAGAAACTTAGTAACATGCTTCATGAGGTGGAGGAGGAGGAGGAAATACAGAAATACAGATGAAAACTTAGTAACATGCTTCATGAGGTGGAGGAGGAGGAGAATGCAAGAAACTTAGTAACATGCTTCATGGTGGAGGAGGGCAGGGGAGGAGCAGCAGCAGCAGCAGCAGCA
6 8 6 8 6	8 6 8 6 8 6 8 6 8	8 8 8	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
Db 1450 TTAGGGCTTCCACCAAATTCTGAAAAC	6642 ence 1337 from Patent W00216655. 6642 6642. 160psis thaliana (thale cress) 160psis thaliana 170psis thaliana	PEATURES (CH) Source 12043 Location/Qualifiers Source / Organism="Arabidopsis thaliana" //mol_type="unassigned DNA" /db_xref="taxon:3702"	Alignment Scores: 1150.50

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                                                                                                                                                                                                                                                                                                                                                                                               Chauk, R., Chan, H., Kim, C.J., Shinn, P., Bowser, L., Carninci, P., Cheuk, R., Chen, H., Kim, C.J., Shinn, P., Ishida, J., Jones T., Kamiya, A., Karlin Neumann, G., Kawai, J., Lam, B., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakutrai, T., Satou, M., Seki, M., Southwick, A., Toriumi, M., Wong, C., Theologis, A. and Ecker, J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (15-MAY-2003) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cheuk, R. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equal to this work as PIs.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN tablàdoplas Full-Length cDNA') : Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL DENBAS: Cheuk, R., Chen, H., Kim, C.J., Shimn, P., Bowesr, L., Chan, M.M., Chang, C.M., Dale, J.M., Hsuan, V.W., Jones, T., Karlin-Neumann, G., Lam, B., Chee, J.M., Lin, J., Miranda, M., Nuyyen, M., Ondersa, C.S., Palm, C.J., Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S., Davis, R.W., Theologis, A., and
Sakurai,T., Satou,M., Seki,M., Southwick,A., Toriumi,M., Wong,C., Wu,H.C., Yamada,K., Yu,G., Yuan,S., Shinozaki,K., Davis,R.W., Arabidopsis ORF clones
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 Arcreceraerreaceerrarecrecececerecagracagrereracegracecaecaa 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IleAsn---HisHisGlyLeuLeuGlnArgMetTrpAsnAsnGlnAspGlnSerGlnGln 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 ValileValProSerSerThrGlyValSerAlaThrSerCysGlyGlyIleThrThrAsp 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173 GlnIleSerPheAsnAsn~------AsnIleSerSerSerSerProArgThr 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 MetAsnProAsnAsnTyrMetGlnGlyTyrThrThrSerAspThrGlnGlnGlnGlnGlnGlnGln 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----GlnHisAlaProLeu-----GlnGlnGln
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306
81
201
159
28
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Matches:
Conservative:
Mismatches:
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                                                                                                                                           codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.17e-74
1150.50
51.81%
40.96%
32.29%
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Pred. No.:
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantes; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantes; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases 1 to 2074)
Stamada, T., Chan, M. M., C., Chang, C. H., Chang, E., Dong, J. M., Goldsmith, A. D., Lee, J. M., Onodera, C. S., Quach, H. L.,
Tang, C., Toriumi, M., Mu, H.C., Yamamura, Y., Yu, G., Bowser, L.,
Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B.,
Lin, J., Meyers, M.C., Miranda, M., Natusaka, M., Nguyen, M., Palm, C. J.,
Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A.,
Arabidopsis Open Reading Frame (ORF) Clones
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                                                                                                                                                                                                                               Arabidopsis thaliana putative homeodomain transcription factor (At2935940) mRNA, complete cds.
                                    |||||||:::
-----CAGAAGAGATATGTGGCT 2016
656 TyrasnargMetGlyTyrGluasnIleaspPheGlnSerGlyAsnLysargPheProThr 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL cDNAs: Yamada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Chen, H., Meuk, R., Jones, T., Karlin-Neumann, G., Kini, C., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.
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18	1447 ACAAGTAACCAAGAAAAGAGCCCAATGGCGGACACTAATTACCATATGAATCCCAATCAC 1506 531 ASDPHESETPHELEUGIYSETPHEASDMETASPASHTHTTHTTHTTHTVAIABPHiSIIE 550	625 GlyLeuProProSerGluAsnLeuAlaMetProValSerGln		Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Saki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A. Arabidopsis Full Length cDNA Clones Unpublished 2 (bases Ito 2572) Yamada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Deng, J.M., Goldsmith, A.D., Lee, J.M., Gondera, C.S., Quach, H.L., Tang, C.C., Toriuni, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Carninci, P., Chen, H., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Sshinn, P., Southwick, A.,
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MetValLeuGlySerLysTyrLeuLysAlaAlaGlnGluLeuLeuAspGluValValAsn 222
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                                                                                                                                                                                                                                                 221 CACGGAAACCCACCGGAGATCTCTGCCGGATCGACGGTGGTCTTCAAACGTTGATCCTC 280
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                                                                                                                                                                                                                                                                                         MetAsnProAsnAsnTyrMetGlnGlyTyrThrThrSerAspThrGlnGlnGlnGlnGlnGln 55
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                                                                                                                                                                                                             --SerAsnAsnAsnIleGlnThrLeuTyrLeu
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Conservative:
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PYMERNKEQAROMGSWEKTPLDQSNEDSASKSTSNQEKS PMADTNYHMNPNHGDLEG
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Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A. Direct Submission
Submitted (02-JAN-2002) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-Length CDNA'): Seki, M., Narusaka, M., Ishida, J., Batcou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.
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Location/Qualifiers
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(FLC-1) as a BamHI/XhoI insert."
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/note="compared to genomic sequence"
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/ecotype="Columbia"
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	RESULT 11 RESULT 11 RESULT 11 LOCUS LOCUS LOCUS DEFINITION Solanum tuberosum BEL1-related homeotic protein 29 (Bel29) mRNA, partial cds. ACCESSION REYMORDS SOLAnum tuberosum (potato) ORGANISM SOlanum tuberosum CNGANISM SUARATOGAYOL3, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; audicotyledons; core eudicots;	asterids; lamids; Solanales; Solanaceae; Solanum. 1 (bases 1 to 2128) 1 (bases 1 to 2128) Interacting transcription factors from the three-amextension superclass regulate tuber formation Plant Physiol. 132 (3), 1391-1404 (2003) 2 (bases 1 to 2128) Chen, H., Rosin, F.M. and Hannapel, D.J. A KNOX protein of potato interacts with several mem family of transcription factors	REFERENCE 3 (bases 1 to 2128) AUTHORS Chen, H., Rosin, F.M. and Hannapel, D.J. AUTHORS Chen, H., Rosin, F.M. and Hannapel, D.J. TITLE Direct Submission JOURNAL Submitted (07-AUG-2001) Department of Horticulture, Iowa State University, 257 Horticulture Hall, Ames, IA 50011-1100, USA FEATURES 1. 2128 COLETION COLOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    at
the bottom of the right arm of the chromosome between the ATHATPAS
                       AC007017 120938 bp DNA linear PLN 11-MAR-2002 Arabidopsis thaliana chromosome 2 clone F11F19 map g6825, complete
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1 (bases 1 to 120938)
1 in, X., Kaul, S., Shea, T.P., Fujii, C.Y., Shen, M., VanAken, S.E., Barnstead, M.E., Mason, T.M., Bowman, C.L., Ronning, C.M., Benito, M.-I., Carrera, A.J., Creasy, T.H., Buell, C.R., Town, C.D., Unpublished
2 (bases 1 to 120938)
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Submitted (09-MAR-2000) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
3 (bases 10.120938)
Town,C.D. and Kaul,S.
Direct Submission
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955 GGGGGAGCAGCAGCGCCGCCGAGATGTCGACGAGGAGCGGCAGGAGCAGCAGCAGCAGAGCTGCAG 1014
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343 TACTTCACAGGCGGCGGCGCCGACGACGTCCAGGCC------384
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NIAS Rice Full-Length cDNA Project Team: Kikuchi.S., Satoh,K.,
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Kishikawa-Hirozane,T., Momura,K., Numasaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,A., Murata,M.,
Cota,Y., Saitoh,H., Saskai,C., Sakai,K.,
Sakazume,N., Sano,H., Saskai,C., Sakai,K.,
Takamara,M., Sano,H., Saskai,C., Sakai,K.,
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Yasunishi,A. and Hayashizaki,Y.
Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, Y., Kojima, Y., Komodo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Murata, T., Miura, J., Miyazaki, A., Mizuno, K., Murasami, K., Murata, M., Najata, T., Nashama, Y., Namiki, T., Narikawa, R., Nikura, J., Nishi, K., Oka, M., Ooka, H., Osato, N., Ota, Y., Otomo, Y., Ryu, R., Saltoh, H., Sakai, K., Sakazume, N., Sano, H., Sano, H., Sano, H., Sadaki, D., Satoh, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugami-Takeda, Y., Tagawa, A., Shiraki, T., Shishiki, T., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Uasanishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A., Yamamoto, M., Yasunishi, A., Yazaki, J., Yonishich, M., Yananda, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Collection, mapping, and annotation of 28K full-length cDNA clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (31-JAN-2003) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
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305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
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/cultivar="Nipponbare"
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                              242 GluSerMetProLeuAlaSerAspValAsnThrAsnSerSerGlyGlyGlyGluSerSer
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URL: http://cdnaol.dna.affrc.go.jp/cDNA/
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Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
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Masuda,H., Miura,J., Mizuno,K., Narikawa,R., Nikura,J., Oka,M.,
Ryu,R., Sugano,S., Sugyyama,A., Suzuki,Y., Teunoda,Y., Ueda,M.,
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and Genome Science Laboratory in Riken Genomic Sciences
Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T.,
Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K.,
Itoh,M., Kagawa,T., Kojima,Y., Kondo,S., Kondo,H., Kawai,J.,
Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kawai,J.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N.,
Ota,Y., Saitoh,H., Sasaki,C., Sakai,K.,
Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K.,
Shinagawa,A., Shiraki,T., Soqabe,Y., Tagami,A., ğ
                  Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 150-5862, Japan (E-mail:eXtkuchi@nias.affrc.go.jp, Tel. 191-29-938-7007, Fas.81-29-838-7007) This clone is one of the 32K full-length cDNA clones from japonica
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/mol type="mRNA"
/cultivar="Nipponbare"
/cultivar="Nipponbare"
/cultivar="15947"
/clone="1023014M03"
Agrobiological Sciences, Department of Molecular Genetics,
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1495 ATGCTCGCCAAGCAACCGGCCTCACCAGGAGCCAGGTACGTAC	1675 AAGGCCAAGGAGAG	118	553 AsnAlaLysLysGlnArgAsnAspMetHisLysPheSerProSerSer
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AK070465 AK070465.1 GI:32980489 FLI_CDNA, CAP trapper. Oryza sativa (japonica cultivar-group) Oryza sativa (japonica cultivar-group) Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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il, J., Akimura, T., Arakawa, T., Carninci, P., Doi, K., ura, J., Akimura, T., Hara, A., Hashizume, W., ura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Hanagaki, T., Hara, M., Hiramoto, K., Hiraoka, T., F., Hotta, T., Iida, Y., Ikeda, R., Imamura, K., India, J., Ishii, Y., Ikeda, R., Imamura, K., Haraohi, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., India, S., Kathikawa-Hirozane, T., Kashimoto, N., Kobayashi, M., A., Kishikawa-Hirozane, T., Kusumegi, T., Li, C., Lu, M., Ia, T., Kojima, K., Kojima, Y., Kondo, J., Murakani, K., Wurata, T., Mura, J., Miyazaki, M., Iah, H., Mateubara, K., Murata, T., Mura, J., Miyazaki, A., Iah, H., Marakami, K., Murata, M., Nishika, T., Nashi, K., Nomura, K., Iaki, R., Ohneda, E., Ohno, M., Ohteuki, K., Oka, M., Ooka, H., Sano, H., Sasaki, D., Satoh, K., Satoh, K., Shibata, K., Idawa, A., Shiraki, T., Satoh, K., Suzuki, K., Suzuki, Y., Tagami, M., Tagami, Takeda, Y., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., H., Yamamoto, M., Waki, K., Xie, Q., Yakaki, J., Yokomizo, S. and M., Math, K., Yazaki, J., Yokomizo, S. and
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e Full-Length cDNA Project Team: Kikuchi,S., Satch,K.,
... Kawagashira,N., Dol,K., Kishimoto,N., Yazaki,J.,
... Kamagashira,N., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
... Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
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Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M.,
Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Msuda,H., Miura,J.,
Mizuno,K., Narikawa,R., Nikura,J., Oka,M., Ryu,R., Sugano,S.,
Sugiyama,A., Mareubara,K. and Murakami,K.
Toshimura,A., Mateubara,K. and Murakami,K.
and Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K.,
Akimura,T., Arakawa,T., Carminci,P., Fukuda,S., Hanagaki,T.,
Hara,A., Hanashizume,W., Hayashida,K., Imotani,K., Ishii,Y.,
Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J.,
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ne is one of the 28K full-length cDNA clones from japonica
hyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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                                  SerMetProLeuAlaSerAspValAsnThrAsnSerSerGlyGlyGlyGluSerSer
                                                                                            ArgGlnLysAsnGluValAlaValGluLeuThrThrAlaGlnArgGlnGluLeuGlnMet
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Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakawura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawi, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AlaAsnIleGlnHisAlaProLeuGlnGlnGlnHisPheValGlyValProLeuProAla 91
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|-----CCTGCGTCACAATGTCACAAGAC-------CCCTCT
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/mol type="mRNA"
/cultivar="Nipponbare"
/db xref="taxon:39947"
/clone="J023054P21"
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Search completed: July 29, 2005, 17:21:49 Job time: 8239 secs

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Adc46618 Thalecres
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Ad002224 Thalecres
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Ad280038 A. thalia
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Aac55946 Eucalyptu
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                                      ADC46618
ADD30786
AD144018
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26-JAN-2001; 2001US-0264647P.
22-JUN-2001; 2001US-0300111P.
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Arabidopsis thaliana
WO200216655-A2
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         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                      The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abloric stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to berwent by the European Patent Office
                                           Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.
                                                                                                               Claim 144; SEQ ID NO 1337; 577pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2043 BP; 627 A; 507 C; 507 G; 402 T; 0 U; 0 Other;
WPI; 2002-304127/34
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203	MetvalbeuGlySerLysTyrLeuLysAlaAlaGlnGluLeuLeuAspGluvalvalAsn 222 ::: CTTGTTAGCTCCAAGTACTTGAAGGCAGCACAAGAGCTTCTTGACGAAGTAGTCAAC 624
223	IlevalGlyLysSerIleLysGlyAspAspGlnLysLysAspAsnSer 238 :::
239	MetAsnLysGluSerMetProLeuAlaSerAspValAsnThrAsnSerSerGlyGly 257
258	GlyGluSerSerSerArgGlnLysAsnGluValAlaValGluLeuThrThrAlaGlnArg 277
278	GingluLeuGlinMetLysEysAalaLysEveuLeuAlaMetLeuGluGluValGluGliArg 297 ::
298	TyrargGlnTyrHisHisGlnWetGlnIleIleValLeuSerPheGluGlnValAlaGly 317
318	IleGlySerAlaLysSerTyrThrGlnLeuAlaLeuHisAlaIleSerLysGlnPheArg 337
338	CysLeuLysAspalailealaGluGlnValLysAlaThrSerLysSerLeuGlyGluGlu 357
358 1036	GluGlyLeuGlyGlyLysIleGluGlySerArgLeuLysPheValAspHisHis 375 ::: :::
376 1096	LeuargGlnGlnargAlaLeuGlnGlnIleGlyMetMetGlnProAsnAla 392
393 1156	TrpArgProGlnArgGlyLeuProGluArgAlaValSerValLeuArgAlaTrpLeuPhe 412
413	GluHisPheLeuHisProTyrProLysAspSerAspLysIleMetLeuAlaLysGlnThr 432
433	GlyLeuThrArgSerGlnValSerAsnTrpPheIleAsnAlaArgValArgLeuTrpLys 452
453	PrometValGluGluMetTyrLeuGluGluValLysAsnGlnGluGlnAsnSerThrAsn 472
473	ThrSerGlyAspAsnLysAsnLysGluThrAsnIleSerAlaBroAsnGluGluLysHis 492 ::::: ::: ::: :::: :::GGATCCATGGAAAAGACTCCTTTGGATCAAAGGAACGAAGGAAG
493	ProllelleThrSerSerLeuLeuGlnAspGlylleThrThrThrGlnAlaGlulleSer 512
51	hrSerThrIleSerThrSerProThrAlaGlyAlaSerLeuHisHisAlaHis 530
531	AsnPheSerPheLeuGlySerPheAsnMetAspAsnThrThrThrThrValAspHisIle 550

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------AACAACAGCAACAATAGCAACAACAACAACAACAACACAAACACAAACACAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 223 IleValGlyLysSerIleLysGlyAspAspGin-----LysLysLysAspAsnSer 238
                                                                                                                                                                                                                                                                                                                                          |||||||||||
| ATGAATCCAACTACTTACGTTCAG---TACACCCAACAAGACAACGACTCGAACAACAAC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 HisPheValGlyValProLeu-------ProAlaValSerLeuHisAspGln 97
                                                                                                                                                                                                                                                                                  The present invention relates to novel environmental stress-responsive promoters (ADB23163-ADB22252) from Arabidopsis thaliana. The promoters are useful in constructing and breeding stress-resistant plants for applications in agriculture and horticulture. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTGAGACGCCCACGCGCAGCAGCCTCTTTAACCCTCTCGTCTCAACAGCAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MetValLeuGlySerLysTyrLeuLysAlaAlaGlnGluLeuLeuAspGluValValAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAACAGCAACATCAACAACAACACCCAGCCTATTCACGTCGGATTCGGGTCCGGACATGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTGATTCCGATGACGCTAAATCCCCAACTATTCTCATCGAAAAAGGGTAGTTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                               ValileValProSerSerThrGlyValSerAlaThrSerCysGlyGlyIleThrThrAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeualaSerGlnLeualaPheGlnArgProIleProThrProGlnHisArgGln-----
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                                                                                                                                                                                                                                                                                                                          MetAsnProAsnAsnTyrMetGlnGlyTyrThrThrSerAspThrGlnGlnGlnGlnGlnGln
                                                                                                                                                                                                                                                                   ----SerAsnAsnAsnIleGlnThrLeuTyrLeu
                                                                                         T; 0 U; 0 Other
                                                                                                                                2043
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Conservative:
Mismatches:
Indels:
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GGTTTACCTCATTGTGATAGCTTGTCGTCCACGCACCATCAGGGTTTCATGCAGACCCAC 1854
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AspGlnGlnMetThrAlaAsnPheHis-----GlyAsnAsnGlyValSerLeuThrLeu
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Reuber TL, Creelman RA,
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                                                                                                     642 LeuSerAsnAspLeuGlySerArgSerGluMetGly.
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Jiang C, Reub
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P-PSDB; ADD30304.
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                                                                             GluGlyLeuGly-----GlyLysIleGluGlySerArgLeuLysPheValAspHisHis
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1735 gaccaggacrcarggcgcaaaggracrcaggaaacaacaarggcgrgrgccrcacgrra 1794
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                                                                                                               ---CAGAAGAGATATGTGGCT
                                 ----GlnAsnTyr
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                                GlyLeuProProSerGluAsnLeuAlaMetProValSerGln----
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germination rate of seeds, vigor of plants and seedlings, or leaf and flower senescence. Sequence information related to the polynucleotides and polypeptides can also be used in bioinformatic search methods. The transgenic plant is useful for growing a progeny plant from a parent plant. This sequence represents one of the cDNAs of the invention.
                                                                                                                                                                                            -----GlnGlnGlnGlnGlnGlyGlyLeuSerLeuSerLeuSerProGlnLeuGlnGln
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| ATCTCCGTACTTCACGGTTATCCTCCGCGCGTGCAGTACAGTCTCTACGGTAGCCACCAA
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|-----GATCCACTCACCAGCAGCCGCG
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                                                                                                                                                         HisGlyAsn------SerAsnAsnAsnIleGlnThrLeuTyrLeu
                                                                                                                                                                                                                              LeuLeuPheLeuAsnSerSerProAlaAlaSerAsnAlaLeuCysHisAlaAsnIle---
                                                                                                                                                                                                                                                                                359 AACAACAACAGTAGTTTCGTTTTCCTCGATTCCCACGCGCCCAAGCGCGAGCCAG
                                                                                                                                                                                                                                                                                                                                   IleAsn---HisHisGlyLeuLeuGlnArgMetTrpAsnAsnGlnAspGlnSerGlnGln
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                                                                             2385
306
80
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                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                    G; 494
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                                                   Sequence 2385 BP; 748 A; 578 C; 565
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1148.50
51.67%
40.96%
32.23%
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                                                                                             Percent Similarity:
Best Local Similarity:
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1153 1273 1393 1453 1567 1033 1093 1213 1333 ------GGATCCATGGAAAAGACTCCTTTGGATCAAAGCAACGAAGAT----- 1609 1624 1684 1798 1852 375 590 337 412 432 512 530 570 317 357 472 277 297 LeuArgGlnGlnArgAlaLeuGlnGlnIleGlyMetMetGln------ProAsnAla GACGAGACAATGATGCAGCCAATAAAT----GCGGATTTCAGCTCCAACGAGAGGTCC GlyGluSerSerSerArgGlnLygAsnGluValAlaValGluLeuThrThrAlaGlnArg --- CCGGTGGAGCTAGGCACGCCAGAGAGA GlnGluLeuGlnMetLystysBAlaLysteuLeuAlaMetLeuGluGluValGluGlnArg TyrArgGlnTyrHisHisGlnMetGlnIleIleValLeuSerPheGluGlnValAlaGly IleGlySerAlaLysSerTyrThrGlnLeuAlaLeuHisAlaIleSerLysGlnPheArg CysLeuLysAspAlaIleAlaGluGlnValLysAlaThrSerLysSerLeuGlyGluGlu GluGlyLeuGly-----GlyLyslleGluGlySerArgLeuLysPheValAspHisHis GluHisPheLeuHisProTyrProLysAspSerAspLysIleMetLeuAlaLysGlnThr ProMetValGluGluMetTyrLeuGluGluValLysAenGluGluGluAenThrAen ThrSerGlyAspAsnLysAsnLysGluThrAsnIleSerAlaProAsnGluGluLysHis ProllelleThrSerSerLeuLeuGlnAspGlylleThrThrGlnAlaGlulleSer ThrserThr11eSerThrSerProThrAlaGlyAlaSerLeuHig-----HigAlaHig AsnPheSerPheLeuGlySerPheAsnMetAspAsnThrThrThrThrValAspHisIle AACGGTGACCTAGAAGGCGTCACTGGAATGCAAGGATGCCCCAAGAGACTAAGAACCAGC GluAsnAsnAlaLysLysGlnArgAsnAspMetHisLysPheSerProSerSerIleLeu SerSerValAspMetGluAlaLysAlaArgGluSerSerAsnLysGlyPheThrAsnPro ACGATGAAGATTCTAGAAGAACGGCAAGGGATAAGATCAGATGGTGGCTAC------CCT Leumet -----AlaAlaTyrAlaMetGlyAspPheGlyArgPheAsp---ProHis 923 GGAGCAGAAGCAGCCGGGAAACGT----1094 358 1334 1394 (513 531 1685 1745 974 298 318 1214 376 393 453 473 1610 258 278 338 1568 493 1625 413 551 571

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The invention describes a transgenic plant comprising a recombinant polynucleotide of any one of more than 500 nucleotide sequences fully defined in the specification or its complement. The method of the defined in the specification or its complement. The method of the chancies to be used to produced a plant having altered traits such as: enhanced tolerance to abiotic stress; glyphosphate tolerance; hormone sensitivity; disease resistance; sugar sensing; early or late flowering; altered flower structure, change in stem bifurcations, altered branching pattern, reduced apical dominance, reduced trichome density; lack of trichomes; reduced ectopic trichome development; altered trichome trichomes; increased root prowth; increased root hairs; altered seed development; altered cell proliferation or cell differentiation; rapid development; premakenture sensescence; increased necrosis; increase in seedling or plant size; decreased plant size; leaf morphology; seed morphology; seed biochemistry; increase in root anthocyanins; increase in plant can search methods. This sequence represents a plant transgenic plant, polynucleotides and polypeptides are useful in bioinformatic search methods. This sequence represents a plant transcription factor related polynucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            311 ------AACAACAGCAACAATAGCAACAACAACAACAACAACAACAAAACACAAAA 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               419 CAGTICGICGGAATACCACTCTCAGGTCACGAAGCTGCTICCATTACAGCCGCCGACAAC 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IleAsn---HisHisGlyLeuLeuGlnArgMetTrpAsnAsnGlnAspGlnSerGlnGln 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 ValileValProSerSerThrGlyValSerAlaThrSerCysGlyGlyIleThrThrAsp 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------GATCCCACTCACCACAAGCCGCG 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HisGlyAsn-----SerAsnAsnAsnAsnIleGlnThrLeuTyrLeu 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 HisPhevalGlyValProLeu--------ProAlaValSerLeuHisAspGln 97
                                                                polynucleotide of any one
in bioinformatic search
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36 MetAsnProAsnAsnTyrMetGlnGlyTyrThrThrSerAspThrGlnGlnGlnGlnGlnGlnGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 LeuLeuPheLeuAsnSerSerProAlaAlaSerAsnAlaLeuCysHisAlaAsnIle---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             137 LeuAlaSerGlnLeuAlaPheGlnArgProIleProThrProGlnHisArgGln-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2385 BP; 748 A; 578 C; 565 G; 494 T; 0 U; 0 Other;
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159
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Matches:
Conservative:
Mismatches:
Indels:
                                                                New transgenic plant comprising a recombinant of more than 500 nucleotide sequences, useful
                                                                                                                                 Disclosure; SEQ ID NO 2671; 435pp; English
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1148.50
51.67%
40.96%
32.23%
                 WPI; 2004-132245/13.
P-PSDB; ADI44209.
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|133 GACCAGGAGCTCATGGCGCAAAGGTACTCAGGAAACAATGGCGTGTCCCTCACGTTA 1972
                                                                                               1973 GÉTTTACCTCATTGTGATAGCTTGTCGTCCACGGACCATCAGGGTTTCATGCAGACCCAC 2032
                                                                                                                                                              2033 CATGGGATTCCTATAGGGAGAAGAGTGAAAATAGGAGAAACAGAGGAATATGGACCCGCC 2092
                                                                                                                                                                                                                              2093 ACCATCAATGGTGGTAGCTCGACCACAACCGCACATTCATCAGCGGCAGCTGCCGCGGCT 2152
                                                                                                                                                                                                                                                                                                ------CAGAGGGATATGTGGCT 2194
AspGlnGlnMetThrAlaAsnPheHis-----GlyAsnAsnGlyValSerLeuThrLeu 624
                                                                GlyLeuProProSerGluAsnLeuAlaMetProValSerGln-----GlnAsnTyr 641
                                                                                                                                                                                                                                                              TyrAsnArgMetGlyTyrGluAsnIleAspPheGlnSerGlyAsnLysArgPheProThr 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transgenic; plant; enhanced tolerance to abiotic stress;
glyphosphate tolerance; hormone sensitivity; disease resistance;
sugar sensing; flowering; flower structure; stem bifurcation;
branching pattern; apical dominance; trichome; stem morphology;
root growth; root hair; seed development; cell proliferation;
cell differentiation; premature sensescence; necrosis; plant size;
leaf morphology; seed morphology; seed biochemistry; root anthocyanin;
plant anthocyanin; light response; shade avoidance; bioinformatic;
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Keddie J,
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                                                                                                                                642 LeuSerAsnAspLeuGlySerArgSerGluMetGly-----
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Ratcliffe O, Adam LJ, Reuber TL,
Dubell AN, Pineda O, Yu G;
                                                                                                                                                                                                                                                                                             2153 TACAATGGGATGAACATACAGAAC----
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                                                                                                                                                                                                                                                                                                                             676 GlnLeuLeuProAspPheVal 682
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CREELMAN R A.
RATCLIFFE O.
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RIECHMANN J L.
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REUBER T L.
KEDDIE J.
BROUN P E.
PILGRIM M L.
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HEARD J E.
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PINEDA O.
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Creelman RA,
Pilgrim ML,
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The present invention relates to an isolated nucleic acid molecule encoding a cell proliferation-related polypeptide. The nucleic acid molecule and the encoded polypeptide, and methods are useful for modulating cell proliferation, senescence, differentiation, development, and stress response in plants, and for producing enhanced food crops. The present sequence represents a cell proliferation-related nucleic acid sequence. The present sequence is published separately from the main body of the specification as EPO data.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 397 AACAACCACAATTCGATGAGCGTT------GCACCAGCACCAGGCCAA-----
                                                                                        for
                                                     New nucleic acid molecule encoding a cell proliferation-related polypeptide, useful for modulating cell proliferation, senescence, differentiation, development, and stress response in plants, and f producing enhanced food crops.
                                                                                                                                                                                                                                                                                                       575 A; 459 C; 463 G; 432 T; 0 U; 0 Other;
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110
225
125
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Matches:
Conservative:
Mismatches:
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                             WPI; 2004-534388/51
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--ATGCAATCTGAGGCCTCACAGGCAATC
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                                                                                                                640 TGGAAGAGTATAAAGCAGAAGGCTCAGAAAGACCAGGCTGAAGCAGGAAAATCAGATAAC
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TCCAACCCACAGGAGTCTACTGCCAATGCTGCACCAGAGATTTCTGCTGCTGAGAACAA
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                                                  SerSerArgGlnLysAsn-----GluValAlaValGluLeuThrThrAlaGlnArgGln
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                                    LeuGlySerLysTyrLeuLysAlaAlaGlnGluLeuLeuAspGluValValAsnIleVal
                                                                                       GlyLysSerileLysGlyAspAspGlnLysLysAsp-----AsnSerMetAsn
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         AACAGAATGAAGAAT
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                                                                            ---AACGCT 1662
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                                                                                                                                      611 ThrAlaAsnPheHisGlyAsnAsnGlyValSerLeuThrLeuGlyLeuPro---ProSer 629
                                                                                                                                                                             630 GluAsnLeuAlaMetProValSerGlnGlnAsnTyrLeuSerAsnAspLeuGlySerArg 649
                                                                                                                                                                                                                    SerGluMetGlySerHisTyrAsnArgMetGlyTyr-----GluAsnIleAspPhe 666
                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant; transcription factor; transgenic plant; abiotic stress tolerance; semotic stress tolerance; cold tolerance; heat tolerance; low nitrogen tolerance; low hosphate tolerance; fungal disease; glyphosate resistance; flowering; fertility; seed development; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New recombinant polynucleotide encoding transcription factor polypeptides, useful for producing transgenic plants with advantageous properties compared to a reference plant.
                                                                                                            CGGTTCATGGCTTACCATTTGTCGGGGCTCGGAAGATAC------
                  GluAsnAsnAlaLysLysLysGlnArgAsnAspMetHisLysPheSerProSerSerlleLeu
                                                         571 SerSerValAspMetGluAlaLysAlaArgGluSerSerAsnLysGlyPheThrAsnPro
                                                                                                591 Leumet AlaAlaTyr Alamet GlyAspPheGlyArgPheAspProHisAspGlnGlnMet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reuber TL;
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Sherman BK;
                                                                    1615 GGCAGCCTCCATGATGCCGTCGCCCATCATTCCGATGAG--
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Keddie JS,
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JL, Haake V, Dubell AN,
GATGACAGCTTCATGAACCTAATG-
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17-DEC-2002; 2002US-0434166P.
24-APR-2003; 2003US-0465809P.
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The present invention relates to novel plant transcription factor proteins (1) and nucleotide sequences (II) (AboGista-AboGS778). The present can be used to produce transgenic plants, which overexpress (II), where the transgenic plant has an altered trait as compared to a concrete can be used to produce transgenic plants, which over plant comprises an altered trait selected from increased tolerance to ablotic stress, increased tolerance to cold, increased tolerance to conditions. Increased tolerance to cold, increased tolerance to cold, increased colerance to low nitrogen conditions, increased tolerance to cold, increased tolerance to low nitrogen conditions, increased tolerance to low nitrogen conditions, increased tolerance to low nitrogen conditions, increased tolerance to unitiple fungal pathogens, increased tolerance to succeed semantivity to AGC, altered sugar sensing, increased tolerance to succeed semantivity to AGC, altered sugar sensing, increased tolerance to succeed sensitivity to AGC, altered sugar sensing, increased tolerance to succeed sensitivity to AGC, altered sugar sensing, increased tolerance to succeed sensitivity to AGC, altered sugar sensing, increased tolerance to succeed sensitivity to AGC, altered succeed sensitivity, altered factoring altered stem morphology, altered vacular tissue structure, reduced fertility, altered forming, altered stem morphology, altered vacular tissue structure, reduced altered trichome structure, altered seed trichome structure, altered seed trichome structure, altered seed trichome structure, altered seed trichome structure, altered cell differentiation, altered cell proliferation, altered cell affected plants, dark altered cell proliferation, altered cell affected plants, dark calced plants, dark seed in the seed blomas; large seedlings, dwarfed plants, dark calced relations, altered seed seed concerns, altered seed ordered sead seconce, abnormal embryo development, altered seed ordered leaf prenyl lipid content, altered seed seed ordered leaf prenyl lipid c

Sequence 1971 BP; 667 A; 360 C; 451 G; 493 T; 0 U; 0 Other;

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Conservative:
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LeuLeuAspGluValValAsnIleValGlyLysSerIleLysGlyAspAspGlnLysLys 235

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ABZ13100 standard; DNA; 1884
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to sugars, altered carbon/nitrogen sensing, early flowering, late flowering, altered flower structure, loss of flower determinacy, reduced fertility, altered shoot meristem development, altered branching pattern, altered stem morphology, altered vascular tissue structure, reduced apical dominance, altered trichome development, altered shoot avoidance, altered seed development, altered shoot avoidance, altered seed development, altered seed call proliferation, altered seed call proliferation, altered cell differentiation, altered plass change, altered sensecence, abnormal embryo development, altered plass change.

Codeth, lethality when overexpressed, altered necrosis patterns, increased blants, dark green leaves, change in leaf shape, increased leaf size and mass, light green or gray leaves, glossy leaves, altered abaxial/adaxial polarity, altered seed coloration, altered seed size, altered seed oil content, altered seed shape, large seed, increased leaf fatty acids, altered seed oil content, altered seed protein content, altered seed oil content, altered seed oil content, altered seed oil content, altered seed oil content, altered seed for protein content, altered seed for printed specification, but was obtained in content content printed specification, but was obtained in content content products of protein content.

Cottent part of the printed specification, but was obtained in cottent contents.
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CysLeuLysAspAlaIleAlaGluGlnValLysAlaThrSerLysSerLeuGlyGluGlu 357
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               HisaspGlnIleAsnHisHisGlyLeuLeuGlnArgMetTrpAsnAsnGlnAspGlnSer 114
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                                                                              115 GlnGlnValIleValProSerSerThrGlyValSerAlaThrSerCysGlyGlyIleThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell with an detecting a profile of expressed polynucleotides in the plant cell production of transgenic plants. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to ablotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.
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                                                                                                            Arabidopsis thaliana; plant; gene; stress; transgenic; ds
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26-JAN-2001; 2001US-0264647P-
22-JUN-2001; 2001US-0300111P.
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The present sequence is a cDNA encoding Arabidopsis thaliana transcription factor homologue. The transcription factors are used to alter the structure and developmental characteristics of plants such as soybean, wheat, corn, potato, corton, rice, oilseed rape, sunflower, alfalfa, sugarcane, turf, banana, blackberry, blueberry, strawberry, raspberry, cartaloupe, cauliflower, cucumber, coffee, eggplant, grapes, mango, lettuce, honeydew, melon, onion, papaya, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, peas, watermelon, rosaceous fruits and vegetable brassicas. The transcription factors are specifically useful for modifying traits associated with plant's pathogen tolerance such as alterations in cell wall composition, trichome number or structure, callose induction, phytoalexin induction, and alterations in the cell death response. Transgenic plants expressing these transcription factors are more tolerant to biotrophic or necrotrophic pathogens such as fund; bacteria, molliques, viruses, nematodes and parasitic higher plants. The transcription factors are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        331 GAGCAACAAAACCGTCAC-------AACAACAACAATAACTCAACTTCAT 375
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                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding plant transcription factor polypeptides, useful for altering the pathogen resistance characteristics of plants, e.g. corn, potato and cotton plants.
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                                                                                                                                                                                                                                                                                                                      Reuber L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1983 BP; 585 A; 464 C; 434 G; 500 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                      Pineda O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1983
237
76
178
190
25
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                      Creelman R, Jiang C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 114-116; 134pp; English.
                                                                                                                                                                  MENDEL BIOTECHNOLOGY INC.
                                                                                                              17-APR-2000; 2000US-0197899P.
22-AUG-2000; 2000US-0227439P.
                                                                                                  99US-0166228P
                                                                 14-NOV-2000; 2000WO-US031418
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45.96%
34.80%
23.13%
                                                                                                                                                                                                                                                                                                                    Ratcliffe O,
                                                                                                                                                                                  HEARD J.
RATCLIFFE O.
CREELMAN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          used in gene therapy
                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-335978/35.
P-PSDB; AAE02525.
                                                                                                                                                                                                                                 JIANG C.
PINEDA O.
REUBER L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                   ADAM L.
 WO200135726-A1
                                                                                                 17-NOV-1999;
                                  25-MAY-2001
                                                                                                                                                                                                                                                                                                                Heard J,
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                                                                                                                                                                                  (HEAR/)
(RATC/)
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Query Match:
DB:
                                                                                                                                                                 (MEND-)
                                                                                                                                                                                                                                                (PINE/)
(REUB/)
                                                                                                                                                                                                                                                                                   (ADAM/)
                                                                                                                                                                                                                                                                                                                                     Adam L;
                                                                                                                                                                                                                                    (JIAN/)
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                 ------ACTCCA 1617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------GCGGCGGTTCTTCATTCCTCTCTTCGGTC------GCGGCGGCTTCT 1683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1759 GTGAACGTCATAAGATTCGGGACCAAACAGACTGGTGACGTGTCTTTACGCTTGGTCTA 1818
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                                                                                                                                                                                                GluThrAsnIleSerAlaProAsnGluGluLysHisProIleIleThrSerSerLeuLeu 500
                                                                                                                                                                                                                                                                                                                                  521 ThralaGlyAlaSerLeuHisHisAlaHisAsnPheSerPheLeuGlySerPheAsnMet 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                561 MetHisLysPheSerProSerSerIleLeuSerSerValAspMetGluAlaLysAlaArg 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    581 GluSerSerAsnLysGlyPheThrAsnProLeuMetAlaAlaTyrAlaMetGlyAspPhe 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/product= "A. thaliana transcription factor homologue"
                                                                                                                                                                                                                                 CCCAACÁÁC-----AATGÁAAACAACTTCACTGTCÁTAÁCGCACAA-----
                                                                                                                                                                                                                                                                                                                                                                                                  541 AspAsnThrThrThrValAspHisIleGluAsnAsnAlaLysLysGlnArgAsnAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ThrGlyLeuThrArgSerGlnValSerAsnTrpPhelleAsnAlaArgValArgLeuTrp
                                                                LysProMetValGluGluMetTyrLeuGluGluValLys-------
                                                                                                                              ------AsnGlnGluGlnAsnSerThrAsnThrSerGlyAspAsnLysAsnLys
                                                                                                                                                                                                                                                                  501 GlnAspGly1leThrThrThrGlnAlaGluIleSerThrSerThrIleSerThrSerPro
                                                                                                                                                                                                                                                                                                                                                                                                                                    -----GAAAACGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      627 ProProSerGluAsnLeuAlaMetProValSerGlnGlnAsnTyrLeuSerAsnAspLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana G418 transcription factor homologue, G965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transcription factor, pesticidal, antimicrobial, gene therapy, pathogen tolerance; trichome structure; callose induction, phytoalexin induction; plant structure; plant development; ss.
                                                                                                                                                                                                                                                                                                                                                                 ACGACGATGACATCGACACACAC----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD06494 standard; cDNA; 1983 BP
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                               1390
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432
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432

75 GIMHI SALAPPOLEUGINGINGINGINERPEVALGIVVALPFOLEUPCALAVESETEU 94 433		Oy 647 Gly 647 Db 1945 GGA 1947 RESULT 10 ADC46618 standard; DNA; 1983 BP. XX X
	GINHiabalaproLeuGinGinGinHiaphevalGiyvalProLeuproAlavalSerLeu	IledaySerAlaLysSerTyrThrGlnLeuAlaLeuHisAlalleSerLysGlnPheArg 337

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Indels:
    23.13$
  Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel transgenic plant having recombinant polynucleotide encoding polypeptide that alters trait of transgenic plant when compared with same trait of another plant lacking recombinant polynucleotide.
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Samaha R;
                                                                                                                                                                                                                                                                                                                                                                                                              Ratcliffe O, Zhang J, Jiang C,
Broun P, Reuber L, Pilgrim M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1983 BP; 586 A; 464 C; 433 G; 500 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein/seed trait altering protein of the invention.
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                                      01-NOV-2002; 2002US-00286264.
                                                                         23-MAR-1999; 99US-0125814P.
22-MAR-2000; 2000US-00533030.
                                                                                                                                                                                                                                                                                                                                                                                                              Riechmann JL,
Yu G, Adam L,
                                                                                                                                                        ä
                                                                                                                                  KEDDIE J.
RIECHMANN J I.
RATCLIRFE O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-765498/72.
                                                                                                                                                                                                                                                                                                                                                   PILGRIM M.
SAMAHA R.
                                                                                                                                                                                             ZHANG J.
JIANG C.
PINEDA O.
HEARD J.
                                                                                                                                                                                                                                                                          YU G.
ADAM L.
BROUN P.
REUBER L.
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15-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                            Keddie J,
                                                                                                                                                                                                                                                                                                                                                                                                                                Heard J,
                                                                                                                                (KEDD/)
(RIEC/)
(RATC/)
(ZHAN/)
                                                                                                                                                                                                             (JIAN/)
(PINE/)
(HEAR/)
(YUGG/)
                                                                                                                                                                                                                                                                                                             (BROU/)
(REUB/)
(PILG/)
(SAMA/)
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1983 237 76 178

Length: Matches: Conservative: Mismatches:

1.72e-58 824.00 45.96% 34.80%

Percent Similarity: Best Local Similarity:

Query DB:	Match:	23.13% Indels: 190 10 Gaps: 25
US-10-	624-201	A-2 (1-688) x ADC46618 (1-1983)
ò	15	AspHisGlnGlnArgHisA
ορ	331	GAGCAACAAAACCGTCACAACAACAACAATAACTCAACTC
ò	35	LeuMetAsnProAsnAsnTyrWetGlnGlyTyrThrThrSerAspThrGlnGlnGlnGln 54
Op	376	
ò	55	GlnLeuLeuPheLeuAsnSerSerProAlaAlaSerAsnAlaLeuCysHisAlaAsnIle 74
Op	432	432
ò	75	GlnHisAlaProLeuGlnGlnGlnHisPheValGlyValProLeuProAlaValSerLeu 94
ΩÞ	433	CCGCAGCAACAACACTTTACATGGCCATCTTCCCC 471
'n	95	95 HisAspGlnIleAsnHisHisGlyLeuLeuGlnArgMetTrpAsnAsnGlnAspGlnSer 114
QQ	472	TCCGATCATCATCAAAACCGAGATATGATC 501
ò	115	GlnGlnValileValProSerSerThrGlyValSerAlaThrSerCysGlyGlyIleThr 134
QQ	502	GGAACCGTCCACGTGGAAGGAGGAAAGGGTTTGTCTTTATCTCTCTCA 549
ò	135	ThrAspLeuAlaSerGlnLeuAlaPheGlnArgProIle147
Dp	550	TCTTCATTAGCCGCAGCTAAAGCCGAGGAATATAGAAGCATTTATTGTGCAGCCGTTGAT 609
ò	148	
QQ	610	
ò	162	LeuSerLeuSerLeuSerProGlnLeuGlnGlnGlnIleSerPheAsnAsnAsn 179
ΩÞ	670	TILL TILL TILL TILL TILL TILL TILL TILL
λo	180	19
Ωp	730	TCATCATCATCTCCCCATGGCGGCTTCTTCATCCATTGGAGGGGATCTAC 780
ò	200	SerSerAsnMetValLeuGlySerLysTyrLeuLysAlaAlaGlnGluLeuLeuAspGlu 219
QQ	781	ACGITGAGGAAITCGAAAIATACGAAACCGGCTCAAGAGITGITGAAGAG 831
ò	220	ValvalasnileValGlyLy8SerileLy8GlyAspAspGlnLy8Ly8AspAsnSerMet 239
QO	832	TTTTGTAGTGTT
ò	240	AsnLysGluSerMetProLeuAlaSerAspValAsnThrAsnSerSerGlyGly 257
QQ	874	AGTAGGAACAACTCAAACCCTAATACTACGGTGGAGGAGGGGGG 921
ò	258	GlyGluSerSerSerArgGlnLysAsnGluValAlaValGluLeuThrThrAlaGlnArg 277
QQ	922	
ò	278	GlnGluLeuGlnMetLysLysBalalysLeuLeuAlaMetLeuGluGluValGluGlnArg 297
qq	982	ATTGAACATCAAAGAAGAAAGTCAAGCTACTATCTATGCTTGAAGAGGTGGACGACGG 1041
ò	298	TyrArgGlnTyrHisHisGlnMetGlnIlelleValLeuSerPheGluGlnValAlaGly 317
q	1042	11
ò	318	IleGlySerAlaLysSerTyrThrGlnLeuAlaLeuHisAlaIleSerLysGlnPheArg 337
qq	1102	

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ADD30786;
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CTAGAGCAGAGTTTGCGTCAGCAACGAGCGTTTCATCATATGGGTATGATGGAGCAAGAG 1341
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                                                                                                                                                                                                                                                                                                                                                                           411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              541 AspAsnThrThrThrThrValAspHisIleGluAsnAsnAlaLysLysGlnArgAsnAsp 560
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CysteulysAspAlaIleAlaGluGlnValLysAlaThrSerLysSerLeuGlyGluGlu 357
                                                                                                                                                                                                                                                  372 ValAspHisHisLeuArgGlnGlnArgAlaLeuGlnGlnIleGlyMetMetGlnProAsn 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PheGluHisPheLeuHisProTyrProLysAspSerAspLysIleMetLeuAlaLysGln 431
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                                                                                                                         ---LyslleGluGlySerArgLeuLysPhe
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                                                                                                                                                                                                                                                                                                                                                                        AlaTrpArgProGlnArgGlyLeuProGluArgAlaValSerValLeuArgAlaTrpLeu
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                                                                                                                            358 GluGlyLeuGlyGly----
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The invention relates to a number of isolated Arabidopsis thaliana cDNA sequences and their encoded proteins which are especially transcription factor related boths's and proteins. The isolated or recombinant plant transcription factor polynucleotides and polypeptides are useful in producing transgenic plants with commercially valuable properties, i.e. modified or alteration with commercially valuable properties, i.e. such as an alteration in a plant growth characteristic, e.g. growth rate, germination rate of seeds, vigor of plants and seedlings, or leaf and polypeptides can also be used in bioinformatic search methods. The transgenic plant is useful for growing a progeny plant from a parent plant. This sequence represents one of the cDNAs of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              316 AIGITATTACCAAATCATCAT---CAAGGTTTTGCTTTCACCGACGAAAACACTATGCAG 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New plant transcription factor polynucleotides and polypeptides, useful in producing transgenic plants with commercially valuable properties, such as an alteration in a plant growth characteristic, e.g. growth rate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35 LeuMetAsnProAsnAsnTyrMetGlnGlyTyrThrThrSerAspThrGlnGlnGlnGlnGln
                                                                                                                                                                                                                                                            transcription factor; transgenic plant; growth rate; senescence; germination rate; plant vigor; seedling vigor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heard JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Riechmann JL, Adam LJ, Dubell AT, Heard JE
Jiang C, Reuber TL, Creelman RA, Pineda O,
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                            Plant yield-related polynucleotide clone G965.
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BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MEND-) MENDEL BIOTECHNOLOGY INC
ADD30786 standard; cDNA; 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-AUG-2001; 2001US-0310847P.
19-NOV-2001; 2001US-0336649P.
11-DEC-2001; 2001US-0338692P.
14-UUN-2002; 2002US-0017468.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-AUG-2002; 2002WO-US025805
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824.00
45.96%
34.80%
23.13%
                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana.
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P-PSDB; ADD30787.
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                                                                                                                                                                                                                                                                                                                                                                                                                    WO2003013227-A2
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Pilgrim ML, J
Broun PE;
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                                                                                                                                15-JAN-2004
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us-10-624-201a-2.rng

AC AD144018; XX DT 22-APR-2004 (first entry) XX DS Plant transcription factor related polynucleotide #1: XX	358 GluGlyLeuGlyGly
1945 GGA 1945 GGA 3017 12 14018	318 IleGlySerAlaLyBSerTyrThrGlnLeuAlaLeuHiBAlaIleSerLyBGlnPheArg 337 :::
627	
	278 GlnGluLeuGlnMetLysLysAalaLysLeuLeuAlaMetLeuGluGluValGluGlnArg 297 982 ATTGAACATCAAGCTACTATCCTTGAAGAGGTGGACGGAC
1792CAGCAAGACGTCA	258 GlyGluSerSerSerArgGlnLysAsnGluValAlaValGluLeuThrThrAlaGlnArg 277
581 1756	240 AsnLysGluSerMetProLeuAlaSerAspValAsnThrAsnSerSerGlyGly 257 :::::: ::: 874 AGTAGGAACAACTCAAACCCTAATACTACGGGGGGGGGG
Qy 561 MetHisLysPheSerProSerSerIleLeuSerSerValAspM	ValValAsnileValGlyLysSerIleLysGlyAspAspGlnLysLysAspAsnSerMet
Qy 541 AspAsnThrThrThrValAspHisIleGluAsnAlaL, Db 1714	200 SerSerAsnMetValLeuGlySerLysTyrLeuLysAlaAlaGlnGluLeuLeuAspGlu 219
521	180 IleSerSerSerProArgThrAsnAsnAsnValThrIleArgGlyThrLeuAspGlySer 199
1684	162 LeuSerLeuSerLeuSerProGlnLeuGlnGlnGlnIleSerPheAsnAsnAsn 179
1	148
Qy 465AsnGlnGluGluGlnAsnSerThrAsnThrSerG	135 ThraspleualaserGinLeualapheGinargProile
452 LyBProMetV 1522 AAACCAATGG	
Qy 432 ThrGlyLeuThrArgSerGlnValSerAsnTrpPhelleAsnA 1162 ACTGGTTTATCCAGAAATCAGGTGTCAAATGTTATGTTCATAAATG	HisAspGlnIleAsnHisHisGlyLeuLeuGlnArgMetTrpAsnAsnGlnAspGlnSer
Qy 412 PheGluHisPheLeuHisProTyrProLysAspSerAspLysI	GlnHisAlaProLeuGlnGlnGlnHisPheValGlyValProLeuProAlaValSerLeu
Oy 392 AlatrpargProGlnArgGlyLeuProGluArgAlaValSerV.	55 GlnLeuLeuPheLeuAsnSerSerProAlaAlaSerAsnAlaLeuCysHisAlaAsnIle 74

nalaargvalargLeuTrp 451 rGlyaspasnlysasnlys 480 elleThrSerSerLeuLeu 500 :|||||||::: CATAACCGCACAA----- 1683 :::||| ------ACTCCA 1689 ------GAAAACGAC 1722 ----- dccccccrrcr 1755 BHIB-----GIY 616 1SerLeuThrLeuGlyLeu 626 TyrLeuSerAsnAspLeu 646 | :::||||||:::||| GCACCTCTTAGCACGACAG 1461 AGAGAAGAAGCAGAAGAA 1581 ----- 1713 1791 MetGlualaLysalaarg 580 ileMetLeuAlaLysGln 431 464 ThrileSerThrSerPro 520 LeuGlySerPheAsnMet 540 LysLysGlnArgAsnAsp 560 TyrAlaMetGlyAspPhe 600 KW transgenic; plant; enhanced tolerance to abiotic stress;
KW glyphosphate tolerance; hormone sensitivity; disease resistance;
KW sugar sensing; flowering; flower structure; stem bifurcation; 11598.

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The invention describes a transgenic plant comprising a recombinant polynucleotide of any one of more than 500 nucleotide sequences fully defined in the specification or its complement. The method of the complement of the specification or its complement. The method of the content of the specification or its complement. The method of the content of the specification or its complement. The method of the content of the sensitivity; disease resistance; sugar sensing; early or late flowering; altered flower structure, change in stem bifurcations, altered branching pattern, reduced apical dominance, reduced trichome density; lack of trichomes; reduced ectopic trichome development; altered stem morphology; increased root growth; increased root hairs; altered seed development; altered cell proliferation or cell differentiation; rapid development; altered cell proliferation or cell differentiation; rapid development; content sense in root anthocyanins; increase in seeding or plant size; leaf morphology; seed morphology; seed biochemistry; increase in root anthocyanins; increase in plant can seed biochemistry; increase in root anthocyanins; increase in plant transgenic plant, polynucleotides and polypeptides are useful in bioinformatic search methods. This sequence represents a plant transgenic plant related polynucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New transgenic plant comprising a recombinant polynucleotide of any one of more than 500 nucleotide sequences, useful in bioinformatic search methods.
branching pattern; apical dominance; trichome; stem morphology; root growth; root hair; seed development; cell proliferation; cell differentiation; premature senescence; necrosis; plant size; leaf morphology; seed morphology; seed blochemistry; root anthocyanin; plant anthocyanin; light response; shade avoidance; bloinformatic; transcription factor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1983 BP; 585 A; 464 C; 434 G; 500 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sherman BK, Riechmann JL, Jiang C, Heard JE, I
Creelman RA, Ratcliffe O, Adam LJ, Reuber TL,
Pilgrim ML, Dubell AN, Pineda O, Yu G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                25-FEB-2003; 2003US-00374780.
                                                                                                                                                                                                                                                                 18-APR-2001; 2001US-00837944.
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824.00
45.96%
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HRAKD J E.
HAAKE V.
CREELMAN R A.
RATCLIFFE O.
ADAM L J.
REUBER T L.
KEDDIE J.
BROUN P E.
                                                                                                                                                                                                                                                                                                 SHERMAN B K.
RIECHMANN J L.
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PINEDA O.
YU G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-132245/13.
P-PSDB; ADI44019.
                                                                                                                                                           US2004019927-A1.
                                                                                                                         Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
Pred. No.:
                                                                                                                                                                                              29-JAN-2004.
                                                                                                                                                                                                                                                                                                                (RIEC/)
(JIAN/)
(HEAR/)
(HAAK/)
(CREE/)
(RATC/)
(REUB/)
(KEDD/)
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(PILG/)
(DUBE/)
(PINE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (XOGG/)
                                                                                                                                                                                                                                                                                                 (SHER/)
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Percent Similarity: Best Local Similarity:

Haake V; Keddie J, Broun PE;

	Query 1 DB:	Match:	23.13 % 12	Indels: Gaps:	190 25	
	US-10-	-624-201A-2	2 (1-688) x ADI4401	18 (1-1983)		
	δ	15 A	<pre>spHisGlnGlnArgHisA ::</pre>	snHisGlyAsnSerAsnAs	AspHisGlnGlnArgHisAsnHisGlyAsnSerAsnAsnAsnAsnIleGlnThrLeuTyr	34
	QQ	331 G	331 GAGCAACAAAACCGTCAC-	AACA	caacaaraacrcaacrcrrcar	375
	δ	35 L	euMetAsnProAsnAsnT	YrMetGlnGlyTyrThrTh	LeuMetAsnProAsnAsnTyrMetGlnGlyTyrThrThrSerAspThrGlnGlnGlnGlnGln	54
	Ωp	376 A	TGTTATTACCAAATCATC	arCaaggititgciti	CACCGACGAAAACACTATGCAG	432
	ò	55 G	lnLeuLeuPheLeuAsnS	erSerProAlaAlaSerA	GlnLeuLeuPheLeuAsnSerSerProAlaAlaSerAsnAlaLeuCysHisAlaAsnIle	74
	qq	432 -				432
	ò	75 G	InHisAlaProLeuGlnG	lnGlnHisPhevalGlyVa	ProbeuProAlaValSerben	94
	Ωp	433 -	 CCGCAGCAAC			471
	ò	95 H	isAspGlnIleAsnHisH	iisGlyLeuLeuGlnArgMe	HisAspGlnIleAsnHisHisGlyLeuLeuGlnArgMetTrpAsnAsnGlnAspGlnSer	114
	q	472 -	TCCGATCATCAT	 AT	CAAAACCGAGATATGATC	501
	ò	115 G	inglnvalllevalPros	erSerThrGlyValSerAl	aThrSerCysGlyGlyIleThr	134
	QQ	502 G	GAACCGTCCACGTGGAAG	: : : GAGGAAAGGGTTTGTCTTT	GGAACCGTCCACGTGGAAGGAAAAGGGTTTGTCTTTATCTCTCTCA	549
	ò	135 T	hrAspLeuAlaSerGlnL	euAlaPheGlnArgPr	ThrAspLeuAlaSerGlnLeuAlaPheGlnArgProlle	147
	qq	550 T	:: CTTCATTAGCCGCAGCTA	AAGCCGAGGAATATAGAAC	 CATTTATTGTGCAGCCGTTGAT	609
	δ	148 -	Δ,	roThrProGlnHisArgGl	ProThrProGlnHisArgGlnGlnGlnGlnGlnGlnGlyGly	161
	qq	610 G	GAACTTCTTCTTCTA	ACGCATCCGCTCATCATCA	GGAACTICTICTICTATAACGCATCCGCTCATCATCATCAATTCAAT	699
_	ò	162 L	euSerLeuSerL	euSerProGlnLeuGlnGl 	LeuSerLeuSerLeuSerProGlnLeuGlnGlnGlnIleSerPheAsnAsnAsn 	179
	ΩÞ	670 C	TTCTTCTTGAGAATTCTT	cricicaacarcarcacca	TCAAGTTGTTGGACATTTTGGT	729
	ον	180 I	leSerSerSerProA	rgThrAsnAsnValThrI]	IleSerSerSerProArgThrAsnAsnValThrIleArgGlyThrLeuAspGlySer	199
	Dp	730 T	CATCATCATCTCCCA	TGGCGCCTTCTTCATCCAT	TGGAGGGATCTAC	780
	λ	200 S	erSerAsnMetValLeuG	1 1 1 1 1 1 1 1 1	SerSerAsnMetValLeuGlySerLysTyrLeuLysAlaAlaGlnGluLeuLeuAspGlu	219
	Ωp	781 -	ACGTTGAGGA	ATTCGAAATATACGAAACC	GGCTCAAGAGTTGTTGGAAGAG	831
	δ	220 V	alvalAsnIlevalGlyL	ysSerIleLysGlyAspAe	ValValAsnIleValGlyLysSerIleLysGlyAspAspGlnLysLysAspAsnSerMet	239
	д	832 T	TTTTGTAGTGTT		dgaagacatttcaagaagaactt	873
	à	240 A	snLysGluSerMetProL	euAlaSerAspValAsnTh	240 AsnLysGluSerMetProLeuAlaSerAspValAsnThrAsnSerSerGlyGly	257
	ΩD	874 A	874 AGTAGGAACAAC	TCAAACCCTAATAC	TACCGGTGGAGGAGGAGGCGGA	921
	δ	258 G	lyGluSerSerSerArgG	lnLysAsnGluValAlaVe	GlyGluSerSerSerArgGlnLysAsnGluValAlaValGluLeuThrThrAlaGlnArg	277
	qq	922 G	dercercerchichicecce	GAACAGCTAATGATAGTCC	rccritercrccscrcarcs	981
	δ	278 G	InGluLeuGlnMetLysi	ysAlaLysLeuLeuAlaMe	GlnGluLeuGlnMetLysLysAlaLysLeuLeuAlaMetLeuGluGluValGluGlnArg	297
	οp	982 A	TTGAACATCAAAGAAGAA	AAGTCAAGCTACTATCTAI	GCTTGAAGAGGTGGACCGACGG	1041
	ò		YrArgGlnTyrHisHisG	lnMetGlnIleIleValLe	TyrArgGlnTyrHisHisGlnMetGlnIleIleValLeuSerPheGluGlnValAlaGly	317
	q	1042 T	ACAACCACTACTGCGAAC	aaatgcaaatggtagtga	CTCATTCGACCAAGTAATGGGT	Н
	<i>⁄</i> o		leglySerAlaLysSerT	YrThrGlnLeuAlaLeuHi	IleGlySerAlaLysSerTyrThrGlnLeuAlaLeuHisAlaIleSerLysGlnPheArg	
	qq	1102 T	Accecececerrecer	ACACGACATTAGCTCAAA		1161

(first entry)

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AD002224 standard; cDNA; 1983
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                       AD002224;
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         ----- 1689
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| GAGGCGGCAGGGGCTGCATCCTCGGGGTTAACCAAAGGGGAAACGCCGCGATTGCGTTTG 1281
                                                                             1282 CTAGAGCAGAGTÍTIGCGTCAGCAACGAGCGTTTCATCATATGGGTATGATGGAGCAAGAG 1341
                                                                                                     GCATGGAGACCGCAACGTGGTTTGCCTGAACGCTCCGTTAATATCCTTAGAGCTTGGCTA 1401
                                                                                                                                    1690 ACGACGATGACATCGACATCAC----- 1713
                                                                                                                                                                                                                                                                                                                                                                      -----GAAAACGAC 1722
                                                                                                                                                                                                                                                                                                                                                                                                                                    1891 CGCCACTCTGGCAATATT-----CCTGATAAGAACACTTCTTTCTCGTTAGAGACTTT 1944
                                                             ValAspHisHisLeuArgGlnGlnArgAlaLeuGlnGlnIlleGlyMetMetGlnProAsn 391
                                                                                                                           PheGluHisPheLeuHisProTyrProLysAspSerAspLysIleMetLeuAlaLysGln 431
                                                                                                                                                           451
                                                                                                                                                                                                                         -----AsnGlnGluGlnAsnSerThrAsnThrSerGlyAspAsnLysAsnLys 480
                                                                                                                                                                                                                                                         481 GluThrAgnIleSerAlaProAgnGluGluLysHisProIleIleThrSerSerLeuLeu 500
                                                                                                                                                                                                                                                                                        501 GlnAspGlyIleThrThrGlnAlaGluIleSerThrSerThrIleSerThrSerPro 520
                                                                                                                                                                                                                                                                                                                                                                                      561 MetHisLysPheSerProSerSerIleLeuSerSerValAspMetGluAlaLysAlaArg 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                     919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   617 AsnAsn------GlyValSerLeuThrLeuGlyLeu 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    627 ProProSerGluAsnLeuAlaMetProValSerGlnGlnAsnTyrLeuSerAsnAspLeu 646
                              GluGlyLeuGlyGly-------LyslleGluGlySerArgLeuLysPhe 371
                                                                                                                                                                                           LysProMetValGluGluMetTyrLeuGluGluValLys----------------------464
                                                                                                                                                                                                                                                                                                                       ThralaGlyAlaSerLeuHisHisAlaHisAsnPheSerPheLeuGlySerPheAsnMet 540
                                                                                                                                                                                                                                                                                                                                                                                                                     581 GluSerSerAsnLysGlyPheThrAsnProLeuMetAlaAlaTyrAlaMetGlyAspPhe 600
CysleulysAspAlaIleAlaGluGlnValLysAlaThrSerLysSerLeuGlyGluGlu 357
                                                                                           AlaTrpArgProGlnArgGlyLeuProGluArgAlaValSerValLeuArgAlaTrpLeu
                                                                                                                                                                                                                                                                                                                                                      AspAsnThrThrThrValAspHisIleGluAsnAsnAlaLysLysGlnArgAsnAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    601 GlyArgPheAspProHisAspGlnGlnMetThrAlaAsnPheHis------Gly
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Thalecress; transcription factor; ss; gene; plant; transgenic; bhosphate tress; cold tolerance, heat tolerance; drought; osmotic stress; phosphate limitation; potassium limitation; nitrogen limitation; hormone sensitivity; disease resistance; sugar sensing; seed germination; flowering; inflorescence architectural change; meristem cell differentiation; phyllotaxy; apical dominance; trichome development; seed development; premature senescence; tathality; necrosis; plant size; leaf morphology; secondary metabolism; light response; shade avoidance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adam LJ, Broun PE;
J C, Samaha RS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kumimoto R;
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Reuber TL, Keddie JS, Yu G, Jiang C,
LL, Creelman RA, Dubell AN, Ratcliffe O,
Thalecress transcription factor cDNA #319.
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30-JAN-2002; 2002US-00958131.
14-JUN-2002; 2002US-00171468.
09-AUG-2002; 2002US-00225066.
09-AUG-2002; 2002US-00225067.
17-DEC-2002; 2002US-043166P.
25-FEB-2003; 2003US-04314166P.
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FROMM M E.
HEARD J E.
RIECHMANN J L.
ADAM L J.
BROIN P E.
PINEDA O.
REUBER T L.
KEDDIE J S.
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JIANG C.
SAMAHA R S.
PILGRIM M L.
CREELMAN R A.
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P-PSDB; AD002225.
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Sherman BK;
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New transgenic plant, useful in developing phenotypes with altered or improved characteristics or traits.

Claim 1; SEQ ID NO 637; 213pp; English.

complementary a sequence encoding a polypopetide, that initiates transcription (i.e. a transcription factor) from Arabidopsis, Soybean, candertain a sequence encoding a polypopetide, that initiates transcription (i.e. a transcription factor) from Arabidopsis, Soybean, and the polypopetide transcription (i.e. a transcription factor) from Arabidopsis, Soybean, AbDO03520 or ADDO03520 and ADDO03550 and ADDO03 invention relates to a transgenic plant comprises a recombinant thalecress transcription factor of the invention.

Sequence 1983 BP; 585 A; 464 C; 434 G; 500 T; 0 U; 0 Other;

	1983	237	9/	178	190	25	
	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:	
	1.72e-58	824.00	45.96\$	34.80%	23.13\$	12	
Alignment Scores:	Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:	

US-10-624-201A-2 (1-688) x ADO02224 (1-1983)

15 AspHisGlnGlnArgHisAsnHisGlyAsnSerAsnAsnAsnAsnIleGlnThrLeuTyr 34	331 GAGCAACAAAACCGTCACAACAACAACAATAACTCAACTTCAT 375
AspHisGlnGlnArgHisA	gagcaacaaaaccgrcac-
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ò	3lnGlyTyrThrThrSerAspThrGlnGlnGl
QQ	376 AIGTIATIACCAAATCATCATCAAGGTTTTGCTTTCACCGACGAAAACACTATGCAG 432
δ	nLeuLeuPheLeuAsnSerSerProAlaAlaSerAsnAlaLeuCys
QQ	432 432
ò	nHisAlaProLeuGlnGlnGlnHisPheValGlyValP
Dp	4
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QQ	0
γ̈́	GlnVallleValProSerSerThrGlyValSerAlaThrSerCysGlyGlyIl
qq	502 GGAACCGTCCACGTGGAAGGAGGAAAGGGTTTGTCTTTATCTCTCTCA 549
ò	135 ThrAspLeuAlaSerGlnLeuAlaPheGlnArgProIle 147
ΩÞ	0
ò	148ProThrProGlnHisArgGlnGlnGlnGlnGlnGlnGlyGly 161
Ω	610 GGAACTICTICTICTAACGCAICCGCICAICAICAICAATICAAICAGAIT 669
ò	162 LeuSerleuSerLeuSerProGlnLeuGlnGlnGlnIleSerPheAsnAsnAsn 179
ф	670 CTICTICITGAGAATICTICTICICACAICATCACCAICAAGTIGIIGGACAITITGGI 729
ò	180 IleSerSerSerSerProArgThrAsnAsnValThrIleArgGlyThrLeuAspGlySer 199
qq	730 TCATCATCATCATCCCATGCGGCTTCTTCATCCATTGGAGGATCTAC 780
ò	O SerSerA
qq	781ACGTTGAGGAATTCGAATATACGAAACCGGCTCAAGAGTTGTTGGAAGAG 831
ò	220 ValvalAsnIleValGlyLysSerIleLysGlyAspAspGlnLysLysAspAsnSerMet 239
QQ	832 TTTTGTAGTGTTGGAAGAGACATTTCAAGAAGAACAAACTT 873
ò	240 AsnLysGluSerMetProLeuAlaSerAspValAsnThrAsnSerSerGlyGly 257
ф	874 AGTAGGAACAACTCAAACCCTAATACTACCGGTGGAGGAGGAGGGG 921
ζ	258 GlyGluSerSerArgGlnLysAsnGluValAlaValGluLeuThrThrAlaGlnArg 277
QQ	922 GGGTCCTCGTCATCGGCCGGAACAGCTAATGATAGTCCTCCTTTGTCTCCGGCTGATCGG 981
δ	278 GlnGluLeuGlnMetLysLysAlaLysLeuLeuAlaMetLeuGluGluValGluGlnArg 297
Вр	ч
'n	298 TyrArgGlnTyrHisHisGlnMetGlnIleIleValLeuSerPheGluGlnValAlaGly 317
οg	-
ò	318 IleGlySerAlaLysSerTyrThrGlnLeuAlaLeuHisAlaIleSerLysGlnPheArg 337
ΩP	11
ò	338 CysLeuLysAspAlalleAlaGluGlnValLysAlaThrSerLysSerLeuGlyGluGlu 357
Ορ	12
γò	358 GluGlyLeuGlyGly
qq	1222 GAGGCGCCAGGGCTGCATCCTCGGGGTTAACCAAAGGGGAAACGCCGCGATTGCGTTTG 1281
ò	372 ValAspHisHisLeuArgGlnGlnArgAlaLeuGlnGlnIleGlyMetMetGlnProAsn 391

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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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99US-0123180P.
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                                       Arabidopsis thaliana
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                                       TTCGAGCATTTTCTTAATCCGTACCCAAGCGATGCTGATAAGCACCTCTTAGCACGACAG
                                                                                                      ThrGlyLeuThrArgSerGlnValSerAsnTrpPhelleAsnAlaArgValArgLeuTrp
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                             AlaTrpArgProGlnArgGlyLeuProGluArgAlaValSerValLeuArgAlaTrpLeu
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63 oAlaAlaSerAsnAlaLeuCysHisAlaAsnIleGlnHisAlaProLeuGlnGlnHi 83
:::::|||:::|||
275 TTCTTCTTCATCCGCCGCGTCATCTTTCACCGTCACGGCGGGGGGGTACTGTTCGAAACGA 334

US-10-624-201A-2 (1-688) x AAC39138 (1-2025)

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2025 222 92 143 173 23

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

3.8e-58 820.00 49.84% 35.24% 23.01%

Score:
Percent Similarity:
Pest Local Similarity:
Query Match:

30 IleGlnThrLeuTyrLeuMetAsnProAsnAsnTyr-WetGlnGlyTyrThrThrSerAs 49

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990XS-0151930P. 990XS-0152363P. 990XS-0153053P. 990XS-0154018P. 990XS-0154018P. 990XS-0154039P. 990XS-0155486P. 990XS-0155486P. 990XS-0155486P. 990XS-0155486P. 990XS-0155486P. 990XS-0155486P. 990XS-0155565P. 990XS-015593P. 990XS-015923P. 990XS-015923P. 990XS-015923P. 990XS-015923P. 990XS-015933P. 990XS-015933P. 990XS-015933P. 990XS-015933P. 990XS-015933P. 990XS-015933P. 990XS-016938P. 990XS-01698P. 990XS-016098P.	3.8e-58
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& a	eGlnArgProIleProThrProGlnHisArgGlnGlnGlnGlnGlnGlnGlnGlyGlyLeuSe 	448 lArgLeuTrpLy8ProMetValGluGluMetTyrLeuGluGluVal
è e	163 rLeuSerLeuSerProGlnLeu	464
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g q ₀	10	15-APR-2004.
දු දු	335 nPheargCysLeuLysAspalailealaGluGinValLysAlaThrSerLeuGl 355	18-SEP-2003;
	yGluGluGluGlyLeuGlyGlyLysgleGluGlySerArgLe	
<u>a</u> a	GGAGAAAGGAGGAGTCGTTGGATGACAACAAGGAGAGAGA	(MEND-) MENDEL BIOTECHNOLOGY INC.
e 6	359 ULYBPREVALABRHISHISHISLEUNTGGINGINATGALAUGINGINILEGIYMEYME 388 :::::::: 1178 CAGGTATTTAGATCAACGGTTGAGACAGCAAAGAGCTTTGCATCAACAGCTTGGAATGGT 1237	Giang Riech
ò	388 tGlnProAsnalaTrpArgProGlnArgGlyLeuProGluArgAlaValSerValLeuAr 408	DR WPI; 2004-330163/30. XX

New recombinant polynucleotide encoding transcription factor polypeptides, useful for producing transgenic plants with advantageous properties compared to a reference plant.

Claim 1; SEQ ID NO 1174; 510pp; English

The present invention relates to novel plant transcription factor proteins (I) and nucleotide sequences (II) (ADOS1534-ADOS378). The sequences can be used to produce transgenic plants, which overexpress (II), where the transgenic plant campared to a sequence can be used to produce transgenic plant compared to a latered trait selected from increased tolerance to abiotic stress, increased dermination in cold, increased tolerance to cheat, increased colorance to lateral, increased colorance to low phosphate conditions, increased tolerance to freezing conditions, increased tolerance to freezing conditions, increased tolerance to freezing conditions, increased tolerance to descent including chugal disease and particularly Expsiphe, Fusarium and Botrytis, increased tolerance to multiple fungal pathogens, increased tolerance to gruphosate, increased tolerance to multiple fungal pathogens, increased tolerance to conditions, increased tolerance to multiple fungal pathogens, increased tolerance to multiple fungal pathogens, increased tolerance to conditions, increased tolerance to multiple fungal pathogens, increased tolerance to multiple fungal pathogens, increased tolerance to complete the carbon/nitrogen sensing, early flowering) attered seme morphology, altered sugar sensing, antiple fungal pathogens attered shoot meristem development, altered branching pattern, consider seme morphology, altered secular tissue structure, reduced apical dominance, altered development, altered seed richome etructure, altered coll profileration, alow growth, altered coll profileration, altered development, altered seed programmed cell profileration, altered development, altered seed programmed cell garmiation, alow growth, fast growth, altered cell profileration, altered development, altered senescence, abnormal embryo development, altered senescence, abnormal embryo development, altered seed profileration, altered seed seed seed seed seed seed, increased leaf wax, increased leaf fatty acide, altered seed coloration, altered seed seed s ftp.wipo.int/pub/published_pct_sequences format directly from WIPO at electronic

Sequence 2458 BP; 751 A; 488 C; 545 G; 674 T; 0 U; 0 Other;

2458 218 83 149 153 Length: Matches: Conservative: Mismatches: Indels: 1.06e-57 816.00 49.92% 36.15% 22.90% Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB: Alignment Scores: Pred. No.:

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رم,	137	137 LeualaSerGlnLeualaPheGlnArgProIleProThrProGlnHisArgGlnGlnGln 156

ą	705	atggtaraaaaggagtgttttacaaccc	 CATGACCCC 743
<i>≿</i>	157	157 GlnGlnGlnGlyGlyLeuSerLeuSerLeuSerProGlnLeuGlnGlnGlnIleS	InIleSerPhe 176
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~	217	17	lnLys 234
ą	834		
λ;	235	6	snThrAsnSer 254
q	867	63	craagarrcr 923
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ą	924	24 garddaaarcraccadrcaarcrarddaargr	STTCCACTGCT 983
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<i>≿</i> ;	307	307	326
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Title: Perfect score:

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Sequence 1833, Ap Sequence 1939, Appl Sequence 139, Appl Sequence 130, Appl Sequence 310, App Sequence 311, App Sequence 1031, App Sequence 185, App Sequence 2195, App Sequence 2156, App Sequence 4, Appli Sequence 2149, App Sequence 2149, App Sequence 227, Appli Sequence 2149, App Sequence 227, Appli Sequence 227, App Sequence 237, Appli Ap
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APPLICANT: Shenk, Michael A.
APPLICANT: Shenk, Michael A.
APPLICANT: McGrath, Annette
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REPERENCE: 11000.1021UJ
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 65
LENGTH: 1239
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US-09-949-016-648

US-09-949-016-3863

US-09-949-016-3863

US-09-313-294A-2156

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Patent No. 6833446
GENERAL INFORMATION:
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ORGANISM: Eucalyptus grandis
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-MODBL=frame+ p2n.model -DEV=xlh
-MODBL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10624201/runat_27072005_122958_10931/app_query.fasta_1.839
-Q=/cgn2_1/USPTO_spool/US10624201/runat_27072005_122958_10931/app_query.fasta_1.839
-DB=Issued_Patents_NA -QFWT=fastap -SUFFIX=rni -MINNATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -GTNATT=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=ptc -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODB=LOCAL -OUTFMT=ptc -NORM=ext -HRAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10624201_@CGN 1 1 177 @runat 27072005 122958 10931 -NCPU=6 -ICPU=3
-NO MAAAP -LARGEQUERY -NGG =CGRESC - WAIT -DSPELOCK=10 -LONGLOG
-DBV INBCOVT=120 -WARN TIMEOUT=0 -TRIREADS=1 -XGAPOP=10 -KGAPORT=0.5 -FCAPOP=6
-FGAPORT=7 -YGAPOP=10 -YGAPORT=0.5 -DELOP=6 -DBLEXT=7
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Sequence 102, Appl
Sequence 102, App
Sequence 1472, Ap
Sequence 1854, Ap
Sequence 1578, App
Sequence 418, Appl
Sequence 418, Appl
Sequence 400, Appl
Sequence 400, Appl
Sequence 111, Appl
Sequence 111, Appl
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3666.965 Million cell updates/sec
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41. /Ggn2_6/prodatcal/ina/6B_COMB.seq:*
42. /Ggn2_6/prodatcal/ina/PCTUS_COMB.seq:*
43. /Ggn2_6/prodatcal/ina/PCTUS_COMB.seq:*
44. /Ggn2_6/prodatcal/ina/PCTUS_COMB.seq:*
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                              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-09-640-211A-172
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US-09-640-211A-418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       435 ThrargSerGlnValSerAsnTrpPheIleAsnAlaArgValArgLeuTrpLysProMet
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APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: Shenk, Michael A.
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REPERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOPTWARE: FastSEQ for Windows Version 4.0
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Matches:
Conservative:
Mismatches:
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                                                                                   Sequence 77, Application US/09640211A
Patent No. 6833446
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493.00
69.15%
54.79%
13.84%
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ORGANISM: Eucalyptus grandis
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1230 GAGGATGGC 1238
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AsnTyrMetGlnGlyTyrThrThrSerAspThrGlnGlnGlnGlnGlnLeuLeuPheLeu
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Patent No. 6833446
GENERAL INFORMATION:
APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REPERENCE: 11000.1021C1U
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SEQ ID NO 1854
LENGTH: 316
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Mismatches:
Indels:
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Matches:
FILE REFERENCE: 11000.1021CIU
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1472
LENGTH: 381
TYPE: DNA
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US-09-640-211A-1472
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Query Match:
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                                 RESULT 3
US-09-640-211A-102
| Sequence 102, Application US/09640211A
| Sequence 102, Application US/09640211A
| Patent No. 6833446
| GENERAL INFORMATION:
| APPLICANT: Wood, Marion
| APPLICANT: Shenk, Michael A.
| APPLICANT: Glenn, Matthew
| TITLE OF INVENTION: Compositions and Methods for the
| TITLE OF INVENTION: Modification of Gene Transcription
| FILE REFERENCE: 11000.1021C1U
| CURRENT APPLICATION NUMBER: US/09/640,211A
| CURRENT APPLICATION NUMBER: 2000-08-16
| NUMBER OF SEQ ID NOS: 2368
| SOFTWARE: FastSEQ for Windows Version 4.0
| LENGTH: 381
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Patent No. 693346
GENERAL INFORMATION:
APPLICANT: Shenk, Michael A.
APPLICANY: McGrath, Annette
APPLICANY: McGrath, Annette
APPLICANY: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
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363 CAGCAAGAGTCCAAA 377
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Query Match:
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 365 GluGlySerArgLeuLysPheValAspHisHisLeuArgGlnGlnArgAlaLeuGlnGln 384
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Query Match:
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                                                                                                                                            400 ProGluArgAlaValSerValLeuArgAlaTrpLeuPheGluHisPheLeuHisProTyr 419
                                                                                                                                                        62 CCCGAGCGATCTGTTTCTGTCTTACGGCTTGGCTATTTGAACATTTTCTTCATCCGTAT 121
                                                                                                                                                                                        420 ProtysAspSerAspLysIleMetLeuAlaLysGlnThrGlyLeuThrArgSerGlnVal 439
                                                                                                                                                                                                        LeuGluGluValLysAsnGlnGluGlnAsnSerThrAsnThrSerGlyAspAsnLysAsn 479
                                                                                                                                                                                                                                                                                                     :::|||||| ||| ||| 242 GTGGAGGCAGAAGTAGAACTAGATCAAATGATAAAACAGGT 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 380 ArgAlaLeuGlnGlnIleGlyMetMetGlnProAsnAlaTrpArgProGlnArgGlyLeu 399
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                                                                                                          2 CGGGCTCTCCCAACAATTAGGCATGATTCAGCAGCATGCTTGGAGGCCACAGAGAGACATT 61
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                                                                                                                                                                                                                                                                                                                                                                            RESULT 6
US-09-640-211A-359
; Sequence 359, Application US/09640211A
; Sequence 359, Application US/09640211A
; Patent NO. 68334916
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: Glenn, Matchew
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Transcription
; FILER REFERENCE: 11000.1021G1U
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT APPLICATION NUMBER: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 359
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                                                                      US-10-624-201A-2 (1-688) x US-09-640-211A-1854 (1-316)
            Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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  Matches:
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420.00
87.38%
76.70%
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87.38%
76.70%
11.79%
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            Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
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223 IleValGlyLysSerIleLysGlyAspAspGlnLysLysAspAsnSerMetAsnLysGlu 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          576 CCCTACACGCGCCTCCAGAGGATATCCCGCCACTTCCGGTGCCTGCATGACGCG 635
                                                                                                                                                                                                                                                                                                                                                   243 SerMetProLeuAlaSerAspValAsnThrAsnSerSerGlyGlyGlyGluSerSerSer 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         336 AACCAAAGGAGCCCCAAAGATGCGGATGGGGGTTCCAAGAACGAAGCATCCTCAAAATCCC 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263 ArgGlnLysAsnGluValAlaValGluLeuThrThrAlaGlnArgGlnGluLeuGlnMet 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LysLysAlalysLeuLeuAlaMetLeuGluGluValGluGlnArgTyrArgGlnTyrHis 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  323 SerTyrThrGlnLeuAlaLeuHisAlaIleSerLysGlnPheArgCysLeuLysAspAla 342
                                                                                                                                                                                                                                                                                                                                                                                                                                 282 ---GIGCGAAAGGCTITGAAGGCTCTGATGACGCGAATGACCAATCTAGACAT---GAG
                                                                                                                                                                                                                                                                                                                                   203 MetValLeuGlySerLysTyrLeuLysAlaAlaGlnGluLeuLeuAspGluValValAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 400. Application US/09640211A
; Sequence 400. Application US/09640211A
; Patent No. 683446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: Glean, Mathew
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Transcription
; FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: PSESEQ for Windows Version 4.0
; SEQ ID NO 400
; LENGTH: 690
                                                                                                                                                                                          Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                            US-10-624-201A-2 (1-688) x US-09-640-211A-37 (1-698)
                                                                                                                                                        Length:
Matches:
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 37 LENGTH: 698
                                                                                                                                                  4.41e-31
360.00
69.23$
47.44$
                                                          TYPE: DNA ORGANISM: Eucalyptus grandis
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US-09-640-211A-400
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PheGluHisPheLeuHisProTyrProLysAspSerAspLysIleMetLeuAlaLysGln 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      372 ValAspHisHisLeuArgGlnGlnArgAlaLeuGlnGlnIleGlyMetMetGlnProAsn 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 CTAGAACGAAGCATACGACACACACGCGCATTTCACCACTTAGGATTGATGGAGCACAC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        392 AlaTrpArgProGlnArgGlyLeuProGluArgAlaValSerValLeuArgAlaTrpLeu
                                            US-09-640-21A-418

Sequence 418, Application US/09640211A

Sequence 418, Application US/09640211A

Patent No. 6833446

GENERAL INFORMATION:

APPLICANT: Wood, Marion

APPLICANT: Shenk, Michael A.

APPLICANT: GONDOSITION:

TITLE OF INVENTION: Compositions and Methods for the

TITLE OF INVENTION: Modification of Gene Transcription

FILE REFERENCE: 11000.1021C1U

CURRENT APPLICANT: 8000.021C1U

CURRENT FILING DATE: 2000-08-16

NUMBER OF SEQ ID NOS: 2368

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 418

LENGTH: 323
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    301 GAAGAAAAGTGGACCAAGGTACACACAATTCTGAAGCTGAA 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     323
74
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Matches:
Conservative:
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411.00
85.05$
69.16$
11.54$
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Pinus radiata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity:
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TrpLysProMetValGluGluMetTyrLeuGluGalLysAsnGlnGluGlnBn--- 469
                                                                                                                                       296 CCAAAGGAGATCACCTCGAGGAACCACGACACCCTGCCATCTCTACTAATTCGGCTTCC 355
                                                                                   62 CAGACAGGGCTCACTAGAAGCCAGGTGCTCGAATTGGTTTATAAATGCTCGAGTTCGGCTT 121
                                                                                                                                                                                                                                                       483 AsnIle----SerAlaProAsnGluGluLysHisProIleIleThrSerSerLeuLeu
                                                                                                                                                                                                                                                                                     242 GGCCTCCAGGACAAGGCCCCCAACTCCAATGAGAACAGC-----ACCAAGAGCTTCAAA
--------SerThrAsnThrSerGlyAspAsnLysGluThr
                                                  GlnThrGlyLeuThrArgSerGlnValSerAsnTrpPheIleAsnAlaArgValArgLeu
                                                                                                                                                                                                                                                                                                                         GlnAspGlyIleThrThrThrGlnAlaGlu-----IleSerThrSerThrIleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1246, Application US/09640211A

Sequence 1246, Application US/09640211A

Patent No. 683344

GENERAL INFORMATION:
APPLICANT: Wood, Marion
APPLICANT: Model Annette
APPLICANT: Glenn, Matthew
CIRLE REFERENCE: 1000.10211U
CURRENT APPLICANTION: Modification of Gene Transcription
FILE REFERENCE: 11000.10211U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1246
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319.50
68.60%
57.02%
8.97%
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                               356 TCC 358
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                                                                                                                                                                                                        217
                                                                                                                                                                                                                         274 GCAGAGCTCTCAAACACTTTAACTGGTTCCAAATATTTTAAAGCAGCACAGCAATTACTT 333
                                                                                                                                                                                                                                                                     AspGluvalvalvanlevalGlyLysSerileLysGlyAspAspGlnLysLysAspAsn 237
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391 TCCCAAACATGGTTTGGTGCAATATCTGACAAAAAGAATATTGCAACTGAAGCTACTACA 450
                                                                                                                                                                                                                                                                                                                                                                                                           AsnSer------SerGlyGlyGlyGluSerSerArgGlnLysAsn 266
                                                                                                                                                                                                                                                                                                                                                                                                                                         451 AATGACCGAACAACATCTGCAATAACAGGAGCTTCAATTTCTGCAGAAGTAATGAAAAC 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GluValAlaValGluLeuThrThrAlaGlnArgGlnGluLeuGlnMetLysLysAlaLys 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         511 GAGCATGCTTTTGGACTCACACCAGCTGATAGACAAGAACTTCAGATGAAAAAGGCAAAG 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuLeuAlaMetLeuGluGluValGluGlnArgTyrArgGlnTyrHisHisGlnMetGln 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            411 LeuPheGluHisPheLeuHisProTyrProLysAspSerAspLysIleMetLeuAlaLys 430
                                                                                                                                    181 SerSerSerFroArgThrAsnAsnValThrIleArgGlyThr---LeuAspGlySer 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           307 ilelleValLeuSerPheGluGlnValAlaGlyIleGlySerAlaLysSerTyrThr 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              200 Ser-----SerAsnMetValLeuGlySerLysTyrLeuLysAlaAlaGlnGluLeuLeu
                                                                                                                                                                                                                                                                                                                                         SerMetAsn------LysGluSerMetProLeuAlaSerAspValAsnThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
US-09-640-211A-111
i Sequence 111, Application US/09640211A
i Sequence 111, Application US/09640211A
i Patent No. 6833446
i GENERAL INFORMATION:
i APPLICANT: Wood, Marion
i APPLICANT: Shenk, Michael A.
i APPLICANT: Glenn, Matthew
i TITLE OF INVENTION: Compositions and Methods for the
i TITLE OF INVENTION: Madification of Gene Transcription
i FILER REFERENCE: 11000.1021C1U
i CURRENT APPLICATION NUMBER: US/09/640,211A
i CURRENT APPLICATION NUMBER: 2000-08-16
i NUMBER OF SEQ ID NOS: 2368
i SOFTWARE: FastSEQ for Windows Version 4.0
i LENGTH: 380
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                 Conservative:
Mismatches:
Indels:
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Conservative:
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Indels:
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                                                                                                     US-10-624-201A-2 (1-688) x US-09-640-211A-400 (1-690)
   Matches:
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319.50
68.60%
57.02%
8.97%
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               61.64%
49.69%
9.22%
                   Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
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Pred. No.:
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DB:
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CAGACAGGCTCACTAGAAGCCAGGTGTCGAATTGGTTTATAAATGCTCGAGTTCGGCTT
                                                              GlnThrGlyLeuThrArgSerGlnValSerAsnTrpPheIleAsnAlaArgValArgLeu
                                                                                                                           451 TrpLysProMetValGluGluMetTyrLeuGluGluValLysAsnGlnGluGlnAsn---
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380 69 14 23 15

Length:
Matches:
Conservative:
Mismatches:
Indels:

Gaps:

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Percent Similarity:
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                 RESULT 14
US-09-640-211A-1845
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LENGTH: 260
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                                                      296 CCAAAGGAGATCACCTCGAGGAACCACGACACCCCTGCCATCTCTACTAATTCGGCTTCC 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------Gregaagaagrecaacagetrcaacacracacacacacacrea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  509 AlaGluIleSerThrSerThrIleSerThrSerPro-----ThrAlaGlyAlaSer 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGAGGAGCAGAGAAAAACCAAGCAAGAGTGAACGCGAGGACTCAGCATCCAAGTCCTCT 241
                                                                                               501 GlnAspGlyileThrThrGlnAlaGlu-----ileSerThrSerThrIleSer 517
                               483 AsnIle-----SerAlaProAsnGluGluLysHisProlleIleThrSerSerLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                493 ProllelleThrSerSerLeuLeuGlnAspGlyIleThrThrGln------
                                                                                                                                                                                                                                                             Sequence 111, Application US/09640211A

Sequence 1121, Application US/09640211A

Batent No. 683346

GENERAL INFORMATION:
APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: Glenn, Matchew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021G1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT PILING DATE: 2000-08-16

NUMBER OF SEQ ID NOS: 2368
SEQ ID NO 1241

LENGTH: 366

LENGTH: 366
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65
19
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16
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Matches:
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297.00
64.62%
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Best Local Similarity:
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TCC 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-640-211A-1241
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182
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367 SerArgLeuLysPheValAspHisHisHisLeuArgGlnGlnArgAlaLeuGlnGlnIleGly 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        387 MetMetGlnProAsnAlaTrpArgProGlnArgGlyLeuProGluArgAlaValSerVal 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 TCCCGTCTTCACTTGTTGATCAACAATACGACAACAGCGGAGCTCTTCAGCAGCTAGGA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        407 LeuArgAlaTrpLeuPheGluHisPheLeuHisProTyrProLysAsp 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1845, Application US/09640211A

Patent No. 6833446

GENERAL INFORMATION:
APPLICANT: Wood, Marion
APPLICANT: McGrath, Annette
APPLICANT: McGrath, Annette
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-640-21A-351

Sequence 351, Application US/09640211A

Sequence 351, Application US/09640211A

Patent No. 6833446

GENERAL INFORMATION:
APPLICANT: Shenk, Maichael A.
APPLICANT: Glenn, Matthew

TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Composition of Gene Transcription
FILE REFERENCE: 11000.1021G1U

CURRENT APPLICATION NUMBER: US/09/640,211A

CURRENT FILING DATE: 2000-08-16

NUMBER OF SEQ ID NOS: 2368

SOFTWARE: PateSEQ for Windows Version 4.0
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Indels:
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256.00
79.49%
69.23%
                                                                                                                                                                                                                                                                                                                                                                                                                                           9.38e-21
260.00
92.86$
83.93$
7.30$
                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA; ORGANISM: Pinus radiata
US-09-640-211A-1845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Pinus radiata
US-09-640-211A-351
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Best Local Similarity:
Query Match:
DB:
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Mon Aug 1 10:58:27 2005
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м	(1-260)	413 GluHisPheLeu-HisProTyrProLysAspSerAspLysIleMetLeuAlaLysGlnTh	.::	432 rGlyLeuThrArgSerGlnValSerAsnTrpPhelleAsnAlaArgValArgLeuTrpLy	TGGACTGACCAGAAGCCAGGTTTCAAATTGGTTTATAAATGCACGTGTCCGCCTTTGGAA 128	452 sProMetValGluGluMetTyrLeuGluGluValLysAsnGlnGluGlnAsnSer	129 ACCCATGGTGGAAGAAATGTATATGGAGGAACTTAGAGGGCCGAAACACAGAATCATGC 188	ThrAsnThrSerGlyAspAsnLysAsnLysGluThr 482	189 AGCAGATTCGAAGGTAACAGAAAGTGGTCAAAGAATGAAGAAAG 237
Gaps:	09-640-211A-351	ProTyrProLysAsp	CCGTACCCAAAAGAT	GlnValSerAsnTrp	CAGGTTTCAAATTGG	MetTyrLeuGluGlu		ThrAsnThrSerGly	ACAACAGAAAGTGGT
4	US-10-624-201A-2 (1-688) x US-09-640-211A-351 (1-260)	GluHisPheLeu-His	CAGCATTCCTTCCAT	rGlyLeuThrArgSer	TGGACTGACCAGAAGC	sProMetValGluGlu	ACCCATGGTGGAAGAA		AGCAGATTCGAAGGTA
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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July 29, 2005, 14:48:42; Search time 1102 Seconds (without alignments)
4040.818 Million cell updates/sec
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3563
1 MYYQGTSDNTNIQADHQQRH......GNKRFPTQLLPDFVTGNLGT 688
OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                            Title:
Perfect score:
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14575566 Total number of hits satisfying chosen parameters: 7287783 segs, 3236178273 residues Searched:

0.5 0.5 0.7

Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su Minimum DB seq length: 0 Maximum DB seq length: 2000000000

summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 1335, A Sequence 1337, Ap Sequence 1337, Ap Sequence 1337, App Sequence 135, App Sequence 135, App Sequence 135, App Sequence 135, App Sequence 1315, App Sequence 1315, App Sequence 13195, A Sequence 13195, A Sequence 13195, A Sequence 13196, A Sequence 13196, A Sequence 13196, A Sequence 13196, App Sequence 131, App Sequence 2319, App Sequence 2154, App Sequence 225, Ap	
SUMMARIES	US-10-424-591-130528 US-10-424-591-130528 US-10-429-130528 US-10-491-918-1337 US-10-2918-842A-1337 US-10-2918-842A-1337 US-10-225-066A-335 US-10-424-599-131558 US-10-424-599-131558 US-10-424-599-131578 US-10-425-114-9882 US-10-425-114-9882 US-10-425-114-9882 US-10-425-114-9882 US-10-425-114-9882 US-10-425-114-9882 US-10-425-114-9882 US-10-425-114-9882 US-10-425-114-1176 US-10-425-114-1176 US-10-425-114-1176 US-10-425-114-1176 US-10-425-114-1176 US-10-425-114-1178 US-10-425-114-1178 US-10-425-114-1178 US-10-425-114-1178 US-10-425-114-1178 US-10-425-114-1178 US-10-425-114-1178 US-10-425-114-1178 US-10-425-114-1178 US-10-425-114-1178 US-10-425-114-1178 US-10-425-114-1178 US-10-425-114-1178 US-10-425-114-1178 US-10-425-114-1178 US-10-425-114-1178 US-10-425-114-1178 US-10-425-114-1178 US-10-425-114-128 US-10-425-114-128 US-10-425-114-28	
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Result No.		

ALIGNMENTS

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Sequence 130628, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associate
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21 (53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 130628

ed With

298 TyrargGlnTyrHisHisGlnMetGlnIleIleValLeuSerPheGluGlnValAlaGly 317	356 GATTGTTAGGAGTTAAGTAGAGGGCGGAGGCTTAGGTTGTTGACCATCTCAGG 415 378 GlnGlnargalaLeuGlnGlnIleGlyMetMetGlnProAsnAlaTrpArgProGlnArg 397 416 CAACAAAGGGCACTTCAGCAGCTAGGAATGATTCAACCAATGCATGGAGGCCCCAAAGA 475	GlyLeuProGluArgAlaValSerValLeuArgAlaTrpLeuPheGluHisPheLeuHis 41 [536 CCTIMICCAAAGGACTCCGATAAAGTTATGCTTGCTAAACTGGACTTGCTAGGACTTGCTAGGAGC 595 438 GlnValSerAsnTrpPheIleAsnAlaArgValArgLeuTrpLysProMetValGluGlu 457 596 CAGGTGTCAAACTGGTTTATCAATGCCCGAGTTTGGAAGCCAATGGTTGAAGAA 655 458 MetTyrLeuGluGluValLysAsnGluGluGluAsnSerThrAsnThrSerGly 475 666 ATGTACTTGAAACTAGAAAGCAATGAAAGGAAATGGTTCAGAAAACA 715	76 AspAsnLysAsnLysGluThrAsnIleSerAlaProAsnGluGlu 16 AAAGAATCGACAAGAGTTGGCTTCAACAGCAAATGTTGCATCGATCATCGATCATCGATCATGATCTTGCATCATCGATCATCGATCATGATGTTGGATCATCTTTGTATCATCATCATCATCATCATCATCATCATCATCATCATC	ThralaGlyalaSerLeuHisHisAlaHis ThralaGlyalaSerLeuHisHisAlaHis : : : : : : ATGGGAGGGTCCCTTCAATCCCACTCT ASPASHTHTHTHTHTVALASPHISILE	### ##################################	584 ASBLY8
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	Qy 641 TyrLeuSerAsnAspLeuGlySerArgSerGluMetGlySerHisTyrAsn 657 1:::	Db 2273 GAGTTTTGTACTATCAACCTGCTCCACCTTCTTCTCACTCA	ESUL 2 S-10-425-114-1 Sequence 133 Publication P GENERAL INFO APPLICANT: APPLICANT: APPLICANT:	ck E leic ants 3313	S	6.33e-107 Length: 1174.50 Matches: 66.06% Conserva 54.42% Mismatch 32.96% Indels: 18	US-10-624-201A-2 (1-688) x US-10-425-114-13353 (1-1555) QY

98 IleasnHisHisGlyLeuLeuGlnargMetTrpasnasnGlnaspGlnSerGlnGln 116 1 1 1 1 1 1 1 1	117 ValileValProSerSerThrGlyValSerAlaThrSerCyeGlyGlyIleThrThrAsp 361 GTG	137 LeuAlaSerGlnLeuAlaPheGlnArgProIleProThrProGlnHisArgGln	155GlnGlnGlnGlnGlyGlyLeuSerLeuSerFeuSerProGlnLeuGlnGln :::	y 173 GlnIleSerPheAsnAsnAsnIleSerSerSerProArgThr 187	y 188 AsnAsnValThrIleArgGlyThrLeuAspGlySerSerSerAsn 202	203	y 223 IleValGlyLysSerIleLysGlyAspAspGlnLysLysAspAspAsnSer 238	y 239 MetasnLysGluSerMetProLeualaSerAspValAsnThrAsnSerSerGlyGly 257	y 258 GlyGluSerSerArgGlnLysAsnGluValAlaValGluLeuThrThrAlaGlnArg 277)y 278 GlnGluLeuGlnMetLysLysAlaLysLeuLeuAlaMetLeuGluGluValGluGlnArg 297	298 TyrargGlnTyrHisHisGlnMetGlnIlelleValLeuSerPheGluGlnValAlaGly 31	y 318 ileglySerAlaLysSerTyrThrGlnLeuAlaLeuHisAlaIleSerLysGlnPheArg 337	338 CysLeuLysAspalaIlealaGluGlnValLysAlaThrSerLeuGlyGluGlu 357	358 GluGlyLeuGlyGlyLysIleGluGlySerArgLeuLysPheValAspHisHis 375 ::: :::	y 376 LeuargGlnGlnargalaLeuGlnGlnIleGlyWetMetGlnProAsnala 392	1293 TrpArgProGlnArgGlyLeuProGluArgAlaValSerValLeuArgAlaTrpLeuPhe 412	y 413 GluHisPheLeuHisProTyrProLysAspSerAspLysIleMetLeuAlaLysGlnThr 432	y 433 GlyLeuThrArgSerGlnValSerAsnTrpPhelleAsnAlaArgValArgLeuTrpLys 452
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Qy 622 LeuThrLeuGlyLeuProProSerGluAsnLeuAlaMetProValSerGlnGlnAsn 640		Qy 659 MetGlyTyrGluAsnile 664 Db 1313 TTTGTACTATCAACACTGCTCCACCTTCTTCTCAGGAACCACTTATGAGAGACATT 1372	Qy 665 AspPheGlnSerGlyAsnLysArgPheProThrGlnLeuLeuProAspPheVal 682	ലശ	; Patent No. US20020160378A1 ; GENERAL INFORMATION: ; APPLICANT: Harper, Jeff ; APPLICANT: Kreps, Joel	APPLICANT: Wang, Xun APPLICANT: Zhu, Tong TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TITLE OF INVENTION: SAME, AND METHODS OF USE	; FILE REFERENCE: SCRIFISOU-3 ; CURRENT APPLICATION NUMBER: US/09/938,842A ; CURRENT FILING DATE: 2001-08-24 ; PRIOR APPLICATION NUMBER: US 60/227,866	PRIOR FILING DATE: 2000-08-24 PRIOR APPLICATION NUMBER: US 60/264,647 PRIOR PILING DATE: 2001-01-16 PRIOR APPLICATION NUMBER: US 60/300,111	0)	; TYFE: DNA ; ORGANISM: Arabidopsis thaliana US-09-938-842A-1337	Alignment Scores: 2.4e-104 Length: 2043 Pred. No.: 1150.50 Matches: 306 Percent Similarity: 51.81% Conservative: 81	40.96* Mismacches: 32.29* Indels: 9 Gaps:	OS-10-824-Z01A-Z (1-888) X US-09-938-842A-1337 (1-2043) OY 22 HisGlyAsnSerAsnAsnAsnAsnAsnAsnIleGlnThrLeuTyrLeu 35	36 MetasnProAsnasnTyrMetGlnGlyTyrThrThrSeraspThrGlnGlnGlnGlnGln	56 LeuLeuPheLeuAsnSerSerProAlaAlaSerAsnAlaLeuCysHisAlaAsnIle	133ANCAACAGCAACAATAGCAACAACAACACACAAACACAAAACACAAACACAAACACA	83 HisphevalGlyValProLeuProAlaValSerLeuHisAspGln	Db 241 CAGTTCGTCGGAATACCACTCTCAGGTCACGAAGCTGCTTCCATTACAGCCGCCGACAAC 300

; PRIOR APPLICATION NUMBER: US 60/227,866 ; PRIOR FILING DATE: 2000-08-24 ; PRIOR APPLICATION NUMBER: US 60/264,647 ; PRIOR APPLICATION NUMBER: US 60/300,111 ; PRIOR FILING DATE: 2001-06-22 ; NUMBER OF SEQ ID NOS: 5379 ; SEQ ID NO 1337 ; LENGTH: 2043 ; TYBE: DMA ; ORGANISM: Arabidopsis thaliana US-09-938-842A-1337	Alignment Scores: 2.4e-104 Length: 2043 Pred. No.: 2.4e-104 Length: 306 Score: 306 Percent Similarity: 51.81 Conservative: 81 Best Local Similarity: 40.96 Mismatches: 201 Query Match: 32.29 Indels: 159 DB: 11 Gaps: 28 US-10-624-201A-2 (1-688) x US-09-938-842A-1337 (1-2043)	Qy 22 HisGlyAsn	LeuLeuPheLeuAsnSerSerProAlaAlaSerAsnAlaLeuCysHisAlaAsnIle	Db 181 AACAACAGTAGTTTCGTTTTCCTCGATTCCCACGCGCGCAGCCAAACGCGAGCCAG 240 Qy 83 HisPheValGlyValProLeu	Qy 98 IleAsnHisHisGlyLeuLeuGlnArgMetTrpAsnAsnGlnAspGlnSerGlnGln 116	Oy 137 LeuAlaSerGlnLeuAlaPheGlnArgProIleProThrProGlnHisArgGln 154	
	Db 1432	Qy 551 GluAsnAsnAlaLysGlnArgAsnAspMetHisLysPheSerFroSerSerIleLeu 570 ::	AlaAlaTyrAlaMetGlyAspPheGlyArgPheAspProHis		Qy 642 LeuSerAmhapLeuGlySerArgserGluMetGly	Oy 656 TyrAsnArgMetGlyTyrGluAsnIleAspPheGlnSerGlyAsnLygArgPheProThr 675	SULT 4 SULT 4 SULT 4 SULT 4 Sequence 1337, Application US/0993 Publication No. US20040009476A9 GENERAL INFORMATION: APPLICANT: Harper, Joff APPLICANT: Kreps, Joel APPLICANT: Rang, Xun APPLICANT: APPLICANT: APPLICANT: STU, TONG TITLE OF INVENTION: STRESS-REGULE TITLE OF INVENTION: STRESS-REGULE FILE REFERENCE: SCRIP1300-3 CURRENT APPLICATION NUMBER: US/05 CURRENT APPLICATION NUMBER: US/05

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Qy 591 LeuMetAlaAlaTyrAlaMetGlyAspPheGlyArgPheAspProHis 606 1675 TTCATGGGTAATTCGGGCAATACCAAATGGATGTCAGATTTGATGTCTCA 1734 Qy 607 AspGlnGlnMetThrAlaAsnPheHisGlyAsnAsnGlyValSerLeuThrLeu 624 Db 1735 GACCAGGGCTCATGGCGTACTCAGGAACGATGCTCAGGAACATGGCGTTA 1794 Qy 625 GlyLeuProProSerGluAsnLeuAlaMetProValSerGlnGlnAsnTyr 641 Db 1795 GGTTTACCTCATTGTGATAGGTTGTCATCAGGACTTCATGGAGACCCAC 1854 Qy 642 LeuSerAsnAspleuGlySerTagGSerGluMetGly	1855 CATGGGATTCCTATAGGGAGAAGAGTG 654	ASQUENCE 153, Application US/10495918 Sequence 153, Application US/10495918 Publication No. US20050009187A1 SEQUENCE INFORMATION: APPLICANT: RIKEN TITLE OF INVENTION: A STRESS-RESPONSIVE PROMOTER AND A GENE CORDING FOR A STRESS-RESPONSIVE PROMOTER TITLE OF INVENTION: A STRESS-RESPONSIVE PROMOTER APPLICATION NUMBER: US/10/495,918 PRIOR FILING DATE: 2004-05-18 PRIOR FILING DATE: 2001-11-19 PRIOR FILING DATE: 2001-11-19 PRIOR FILING DATE: 2001-11-19 PRIOR FILING DATE: 2001-11-19 NUMBER OF SEQ ID NOS: 166 Arabidopsis t Arabidopsis t	
625 GCTGATTCCGATGACGCTAAATCCCAACTATTCTCATCGAAAAGGGTAGTTGC 684 239 MetABBLy8GluSerMetProLeuAlaSerAspValAsnThrAsnSerSerGlyGly 257		376 LeuargdinGinargalaLeuGinGinileGiyWetMetGinProAsnala 392	453 ProMetValGluGluMetTyrLeuGluGluValLysAsnGlnGluGluAgnSerThrAsn 472 1336 CCAATGGTGGAGGAAATGGAGGAAATGAAGGCAAAGAACATG 1389 473 ThrSerGlyAspAsnLysAsnLysGluThrAsnIleSerAlaProAsnGluGluLysHis 492 1390GGATCCATGGAAAAGGATCCTTTGGATCAAGGAAGAT 1431 493 ProIleIleThrSerSerLeuLeuGlnAspGlyIleThrThrThrGlnAlaGluIleSer 512 1432TCTGCTTCAAAGTCA 1446 513 ThrSerThrIleSerThrSerProThrAlaGlyAlaSerLeuHisHisAlaHis 530 1447 ACAAGTAACCAAGAAAAGGCCCAATGGCGGACACTAATTACCATTATATATA

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APPLICANT: MENCHED Biotechnology, Inc.

APPLICANT: MADAW, Luc J

APPLICANT: DUBELL, Arnold T

APPLICANT: DUBELL, Arnold T

APPLICANT: DUBELL, Arnold T

APPLICANT: REUBER, T. Lynne

APPLICANT: REUBER, T. Lynne

APPLICANT: REUBER, T. Lynne

APPLICANT: REUBER, T. Lynne

APPLICANT: PINEDA, Cai-Znon

PRIOR FILING DATE: Z001-04-18

PRIOR FILING DATE: Z001-04-18

PRIOR FILING DATE: Z001-12-11

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APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: POLYNUCLECTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBI -0047 CIP
CURRENT APPLICATION NUMBER: US/10/374,780A
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: 09/837,944
PRIOR FILING DATE: 2001-04-18
PRIOR PILING DATE: 2001-04-19
PRIOR PILING DATE: 2001-08-29
PRIOR PILING DATE: 2001-08-29
PRIOR PILING DATE: 2001-11-19
PRIOR PILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR PILING DATE: 2001-11-19
PRIOR PILING DATE: 2001-11-19
PRIOR PILING DATE: 2001-11-19
PRIOR PILING DATE: 2001-12-11
PRIOR PILING DATE: 2001-05-6-14
PRIOR PILING DATE: 2002-06-19
PRIOR PILING DATE: 2002-06-09
NUMBER OF SEQ ID NOS: 2906
SOOTHWAND PATE: 2002-206-09
NUMBER OF SEQ ID NOS: 2906
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Mismatches:
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ORGANISM: Arabidopsis thaliana
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Best Local Similarity:
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LENGTH: 2385
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1145 GACGAGACAATGATGCAGCCAATAAAT-----GCGGATTTCAGCTCCAACGAGAAGCTC 1798
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                                          ThrSerGlyAspAsnLysAsnLysGluThrAsnIleSerAlaProAsnGluGluLysHis
                                                                               ------GGATCCATGGAAAGACTCCTTTGGATCAAAGCAACGAAGAT----
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       1514 CCAATGGTGGAGGAGATGTACATGGAGGAAATGAAGGAGCAGGCAAAGAACATG---
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Publication No. US20040019927A1
GENERAL INFORMATION:
APPLICANT: Sherman, Jose Luis
APPLICANT: Riechmann, Jose Luis
APPLICANT: Heard, Jacqueline E
APPLICANT: Heard, Jocqueline E
APPLICANT: Haake, Volker
APPLICANT: Ratcliffe, Oliver
APPLICANT: Ratcliffe, Oliver
APPLICANT: Adam, Luc J
APPLICANT: Reuber, T. Lynne
APPLICANT: Reuber, T. Lynne
APPLICANT: Reuber, James
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Broun, Pierre E
Pilgrim, Marsha L
Dubell III, Arnold T
Pineda, Omaira
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                                                                                                                 GlyGluSerSerSerArgGlnLysAsnGluValAlaValGluLeuThrThrAlaGlnArg 277
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                                                                                                                              AsnPheSerPheLeuGlySerPheAsnMetAspAsnThrThrThrThrValAspHisIle 550
                ---LysLysAspAsnSer 238
                                        GCTGATTCCGATGACGTAAACGCTAAATCCCAACTATTCTCATCGAAAAAGGGTAGTTGC
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|ATGAATCCAACTACTTACGTTCAG---TACACCCAACAAGACAACGACTCGAACAACAAC 310
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PRIOR APPLICATION NUMBER: 60/310,847
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 60/338,692
PRIOR FILING DATE: 2001-12-11
PRIOR PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 1122
SOFTWARE: Patentin version 3.1
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ORGANISM: Arabidopsis thaliana
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ValasphishishisLeuargGlnGlnargalareuGlnGlnIleGlyMetMetGlnProAsn GTTGATCATCATCAACTGGGACAACGTGCATTACAACAGCTTGGAATGATCCAACAAT AlaTrpargProGlnakrgGlyLeuProGluargalavalSerValLeuargAlaTrpLeu	1aArg
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	Alignment Scores: 1078.00 Score: 1078.00 Score: 1078.00 Score: 1078.00 Score: Percent Similarity: 64.10* Conservative: 57 Best Local Similarity: 18.26* Matches: 102 Best Local Similarity: 18.26* US-10-624-201A-2 (1-688) x US-10-425-114-7804 (1-1606) US-10-624-201A-2 (1-688) x US-10-425-114-7804 (1-1606) Oy 253 AsnSerSerGlyGlyGlyGlySerSerArgGlnLysAsnGluValAlaValGlu 271 :::

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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRENCE: 38-21 (53221) B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 60154
LENGTH: 3029
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US-10-437-963-60154
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nLysArgPheProThrGlnLeuLeuProAspPheVal
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1.2-10-437-963-60154
1. Sequence 60154, Application US/10437963
1. Publication No. US20040123343A1
                                                                          GENERAL INPORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wei
APPLICANT: Wei
APPLICANT: Boutharov, Andrey A.
APPLICANT: Barbazuk, Brad
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ORGANISM: Oryza sativa
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| AAAACCTTAGGTGAAGATGATTGCTTGGGAGTTAAGGTAGAAGGTTCGAGGCTTAGGTAT
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| CAGGATAACACCACAAAAAGATCAAAGCAAAGGAAGGAGTTATGGT-------
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                   Length:
Matches:
Conservative:
Mismatches:
Indels:
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1 Sequence 63874, Application US/10424599

2 Sequence 63874, Application US/10424599

3 GENERAL INFORMATION:

3 APPLICANT: La Rosa Thomas J

4 APPLICANT: Kovalic David K

3 APPLICANT: Zhou Yihua

4 APPLICANT: Zhou Yihua

5 TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

7 TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

7 TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

7 TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

7 TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

7 TITLE OF INVENTION NUMBER: US/10/424,599

7 CURRENT PALLING DATE: 2003-04-28

7 NUMBER OF SEQ ID NOS: 285684
                                                                           GACAGTGCCGCGAAGATGGACAGCAAAGCGGCGCACATGGAGAGCGCGCGGCGGCGTACAT 2450
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                                         ------GluThrAsnIleSerAlaProAsnGluGluLysHisProlleIleThr 496
                                                                                                                                   SerSerLeuLeuGln-AspGlyIleThrThrThrGlnAlaGluIleSerThrSerThrIl 516
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_28692C.1
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2 TYTTYrGlnGlyThrSerAspAsnThrAsn1leGlnAlaAspHisGlnGlnArgHisAsn 21	HisAlaProLeuGlnGlnHisPhevalGlyValProLeuProAlaValSerLeuHis	SCGCCGTCGGGGCTACAACCTGTGGACCCCGGCCATGGCTGGC		ThrasnserserglyGlyGluSerSerArgGlnLysAsnGluVal :::	289 AlaMetLeuGluGluValGluGlnArgTyrArgGlnTyrHisHisGlnMetGlnIleIle 308
> 8 > 8 > 8 > 8	88888	8 8 8 8 8	8 6 8 6 8 6 8	6 6 6 6	3 3 4 5 6 6 6 6 7 6 7
Db 912 GCAAAGCCCAAACAAGCCAATTAGAAGCACTTCTGAAATGCAGAAC			RESULT 13 US-10-425-114-15195 ; Sequence 15195, Application US/10425114 ; Publication No. US20040034888A1 ; GENERAL INFORMATION: ; APPLICANT: Liu, Jingdong ; APPLICANT: Kovalic, David K. ; APPLICANT: Screen, Screen E ; APPLICANT: Tabaska, Jack E ; APPLICANT: Tabaska, Jack E ; APPLICANT: Cao, Yongwei ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement	FILE REFERENCE: 38-21(53313)B	COTHER INFORMATION: Clone ID: LIB3060-003-B11_FLI US-10-425-114-15195 Alignment Scores: Pred. No.: Score: Score: Pert Local Similarity: S6.21* Conservative: Best Local Similarity: 28.04* Indels: DB: US-10-624-201A-2 (1-688) x US-10-425-114-15195 (1-2313)

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                                                                                                            AspGlnIleAsnHisHisGlyLeuLeuGlnArgMetTrpAsnAsnGlnAspGlnSerGln 115
                                                                                                                                                                                                                                                                                                                                                                    GinValIleValProSerSerThrGlyValSerAlaThrSerCysGlyGlyIleThrThr 135
                                                                                                                                                                                                                                                                                                                                                                                                                         136 AspLeuAlaSerGlnLeuAlaPheGlnArgProIleProThrProGlnHisArgGlnGln 155
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                                          TyrTyrGlnGlyThrSerAspAsnThrAsnIleGlnAlaAspHisGlnGlnArgHisAsn 21
                                                                                           22 HisGlyAsnSerAsnAsnAsnIleGlnThrLeuTyrLeuMetAsnProAsnAsnTyr
                                                                                                                                                 42 MetGlnGlyTyrThrThr----SerAspThrGlnGlnGlnGlnGlnLeuLeuPhe
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                US-10-624-201A-2 (1-688) x US-10-425-115-97705 (1-2970)
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Sequence 97705, Application US/10425115

Fublication No. US20040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Cao, Yongwei

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: USBATE

TITLE OF INVENTION: USBATE

TITLE OF INVENTION: USBATE

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CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

SEQ ID NOS: 369326

SEQ ID NOS: 369326

SEQ ID NOS: 2003-04-28

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1959 CAGGACGCTGGAGGCGGCGAACGACGAGGCAAGTCCGGTGGCGGCGGCGGCAGCAGAGC 2018
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                                                                                           GlyMetMetGlnProAgnAlaTrpArgProGlnArgGlyLeuProGluArgAlavalSer 405
                                                                                                                                                 ValLeuArgAlaTrpLeuPheGluHisPheLeuHisProTyrProLysAspSerAspLys 425
                                        GlySerArgLeuLysPheValAspHisHisLeuArgGlnGlnArgAlaLeuGlnGlnIle 385
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Score: Percent Similarity: 63.72% Conservative: 44 Best Local Similarity: 53.49% Mismatches: 90 Query Match: 18 Gaps: 14 US-10-624-201A-2 (1-688) x US-10-425-114-9882 (1-1716) Qy 106 Gln1leileValLeuSerPheGluGlnValalaGlySeralaLysSerTyrThr 325 Db 2 CAAATTGTGGTATCATTAGAGCAAGCAGGGGGTATGGGGCAAAATCTTACACT 61	326 GlnLeublaLeuHisAlaileSerLysGlnPheArgCysLeuLysAspAlaileAlaGlu 62 GCCTTGCCTAAAAACTATCTCAAAGCAATTCAGGTGCTGCTGAAAGATGCCAATCTGGA 346 GlnValLysAlaThrSerLysSerLeuGlyGluGluGluGluGluGluGluGluYLi::	Oy 366 GlySerArgLeuLysPheValAspHisHisLeuArgGlnGlnArgAlaLeuGlnGlnIle 385	Db 302 ATTCTTCGGGCTTTTTGGGCATTTCCTTCACCCATATCCAAAGGACTCCGATAAA 361 Qy 426 IleMetLeuAlaLysGlnThTGJYLeuThArgSerGlnValSerAsnTrpPheileAsn 445 Db 362 GTTATGCTTGCTAAACTGGACTTTCTAGGAGGCCAGGTGTCAAACTGGTTTATCAAT 421 Qy 446 AlaArgValArgLeuTrpLysProMetValGluGluMetTyrLeuGluGluValLysAsn 465		542 503 602 618 659	Qy 538 PheAsnMetAspAsnThrThrThrThrValAspHisIleGluAsnAsnAlaLysGln 557 :::	577
Db 1898 CTGCGCACCATCTCGCGGCAGTTCCGGTGTCTGCGGGACGCGATCGCGAGGTGCGC 1957 Qy 349 AlaThrSerLysSerLeuGlyGluGluGluGlyLeuGlyGlyLysIleGlu 365		Db 2198 ATCATGCTCGCCAAGCAAACCGGGCTCACCAGGAGTCGTCCAATTGGTTCATCAAT 2257 Qy	Qy 482 ThrAsnIleSerAlaProAsnGluGluLysHisProIleIleThrSerSerLeuLeuGln 501 1::::: Db 2378 AGGACACGGTCATGCCGAGGGCGACGTGATGTCCAAGTCCGCGGTGCGC 2437 Qy 502 AspGly	512		; APPLICANT: Tabaska, Jack E ; APPLICANT: Cao, Yongwei ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement ; FILE REFERENCE: 38-21(53313)B ; CURRENT APPLICATION NUMBER: US/10/425,114 ; CURRENT FILING DATE: 2003-04-28 ; NUMBER OF SEQ ID NOS: 73128	SEQ ID NO 9882 DENGTH: 1716 TYPE: DNA ORGANISM: Glycine max FEATURE: OTHER INFORMATION: Clone ID: 700875318_FLI US-10-425-114-9882 Alignment Scores: Pred. No.: 8.51e-88 Length: 1716

Search completed: July 29, 2005, 19:19:10 Job time : 1191 secs

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GST343679
OG1FCC005
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GR EA22F
57778 1 1 55
GA32EN000
Arabidops
EST411755

protein

Σ

Run on:

Sequence:

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685 bp mRNA linear EST 18-MAY-2001
EST278301 tomato callus, TAMU Lycopersicon esculentum cDNA clone
AM01461, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lycopersicon esculentum (tomato)
Lycopersicon esculentum
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (baees 1 to 685)
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T.,
Holt,I.E., Liang,F., Upcon,J., Craven,M.B., Bowman,C.L., Ahn;S.,
Romning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
Giovannoni,J.
Giovannoni,J.
Unpublished (1999)
            A1773253

CC2411755

BIS521008

BRS552737

BRIT76426

AW688195

BRIT76426

AW688195

CO118735

CO118735

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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Lycopersicon esculentum"
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CB671354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                      1 MYYQGTSDNTNIQADHQQRH.....GNKRFPTQLLPDFVTGNLGT
           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                       nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                     34239544 seqs, 19032134700 residues
                                                                                                                                                                                                                                                                            of hits satisfying chosen parameters:
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Maximum Match 100%
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BG593861
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AW930221
BG129304
CO909070
BQ119770
CL978605
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                                                                                                                                                                                         Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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Perfect score:
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981.5
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963.5
                                                                                                                                                                             Scoring table:
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Database

œ Result

PP_LEa001 8aj54b05. NF101F03P MCT026E10 OSJNEe040

BP034454 OBIFCC034

EST311444 Bam70e12

EST245847 EST513701 EST616787 EST513822 RTK1 27 A EST264060

Total number

Searched:

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Solanum tuberosum (potato)

Solanum tuberosum

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; lamids; Solanales; Solanaceae; Solanum.

Is (bases 1 to 756)

Solanales; Solanales; Solanaceae; Solanum.

Solanales; Solanales; Solanales; Solanum.

Chiemingo, A.,

Bougri, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B.

Generations of ESTs from sprouting potato eyes

Unpublished (2000)

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr. Rockville, MD 20850, USA

Email: potato-array@tigr.org

This clone can be obtained from the University of Arizona Genomics

Institute. Orders can be made through URL:

http://genome.arizona.edu/orders/

Seq primer: M15F-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone lib="cSTS"
/note="Vector: pBluescript SK(-); Site 1: BCORI; Site 2:
XhoI; Various sizes of sprouting eyes (Zmm to 15mm) were
taken from tubers. The tubers were incubated at 26C in the
dark for 2-3 weeks prior to sprouting. The eyes were
trozen in liquid nitrogen immediately upon removal from
tubers."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           299 TCTTCACCAGCAGCAGCAAGCAAACGCGCTTTGCCATGCGAATATACAACAACGCGCCGCTGCAA 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 ATGTACTATCAAGGAACCTCGGATAATACTAATATACAAGCTGATCATCAACAACATCAT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 HisGlyLeuLeuGlnArgMetTrpAsnAsnGlnAspGlnSerGlnGlnValIleValPro 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 AsnHisGlyAsnSerAsnAsnAsnAsnIleGlnThrLeuTyrLeuMetAsnProAsnAsn
'n
 Solanum tuberosum cDNA clone cSTS5P9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="sprouting eyes from tubers"
/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
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210
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                            1. 756
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/cultivar="Kennebec"
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99.06%
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                 mRNA sequence.
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Best Local Similarity:
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DB:
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AUTHORS
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/note="Vector: pBlueScript SK(-); Site_l: EcoRl; Site_2:
Xhol; supplier: Giovannoni laboratory; CiEC - Cotyledons
of seedlings 7-10 days post-germination were excised, cut
at both ends and placed on MS medium with no selection.
Mixed callus was harvested at 25 and 40 days and included
undifferentiated masses. Tomato Callus EST Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AlaLeuGlnGlnIleGlyMetMetGlnProAsnAlaTrpArgProGlnArgGlyLeuPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGACGAATATAAGTGCTCCAAATGAAGAGAAACAACCAATTATTATTACTAGCAGCTTATTA
                                                                                                                                                                                                                                                                                                                                                                            321 AlaLysSerTyrThrGlnLeuAlaLeuHisAlaIleSerLysGlnPheArgCysLeuLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                AspalallealagluglnVallysAlaThrSerLysSerLeuGlyGluGluGluGlyLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 GAAAGAGCTGTCTGTCCTTCGTGCTTTGGCTTTTTCGAGCATTTTCTTCATCCTTACCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AsnTrpPhelleAsnAlaArgValArgLeuTrpLysProMetValGluMetTyrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GluGluValLysAsnGlnGluGlnAsnSerThrAsnThrSerGlyAspAsnLysAsnLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GluThrAsnIleSerAlaProAsnGluGluLysHisProIleIleThrSerSerLeuLeu
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/lab_host="XL1-Blue MRF'"
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/lab host="bhlos-TonA"
/clocallb="potato abjotic stress cDNA library"
/clocallb="potato abjotic stress cDNA library"
/note="Vector: pCMVSport6.1; Site 1: ECORI; Site 2: Not1;
supplier: Solanum tuberosum var. Kennebec plants were
grown from cuttings on a 16hr light/8 hr dark cycle at 25
C for 3-4 weeks. Abjotic stress conditions were applied to
the soil with 150 mM NaCl and tissues were harvested at
following application of the salt stress (leaves: 2hr,
6hr, 12hr, 1d, 2d, and 4d; roots:2hr, 6hr, 12hr, and 2d).
Set 2 were grown under the standard conditions and then
were water stressed by withdrawal of further watering
applications. Drought stressed plants were harvested after
cessation of watering (leaves: 3d, 5d, and 7d; roots:3d
and 5d). Set 3 were grown under the standard conditions
and then were cold stressed by placement at 4 C. Cold
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
                                                                                                                                                                                                                                                                                                                                                                                               964 bp mRNA linear EST 03-AUG-2004
BST708180 potato abiotic stress cDNA library Solanum tuberosum cDNA
CLONE POABE14 5' end, mRNA sequence.
                                                   140
                                                                                                                                                                                  GlyLeuSerLeuSerLeuSerProGlnLeuGlnGlnGlnIleSerPheAsnAsnIle 180
                                                                                                                                                                                                                                                   200
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum.
I (bases I to 864)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
Generation of ESTs from abiotic stressed potato tissue
Other ESTs: EST708181
                                                                                                                   160
                                                                                                                                                                                                                    658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The Institute for Genomic Research 9712 Medical Center Dr, Rockville, MD 20850, USA Email: potato-array@tigr.org Clones can be requested from the University of Arizona Genomics Institute via http://genome.arizona.edu/orders/ . Seg primer: ATT TAG GTG ACA CTA TAG.
LeuAlaPheGlnArgProIleProThrProGlnHisArgGlnGlnGlnGlnGlnGlnGl
                                                  SerSerThrGlyValSerAlaThrSerCysGlyGlyIleThrThrAspLeuAlaSerGln
                                                                                                                                      TTGGCGTTTCAGAGGCCGATTCCGACACCCAAACACCGACAGCAGCAGCAACAACAGCAGGC
                                                                                                                                                                                                     GGTCTATCTCTAAGCCTTTCTCCTCAGCTACAACAGCAAATTAGTTTCAATAACAATATT
                                                                                                                                                                                                                                                  SerSerSerProArgThrAsnAsnValThr1leArgGlyThrLeuAspGlySerSer
                                                                                                                                                                                                                                                                                  rcarccrcarccaaggacaarrargrracrarraggggaagarcr
                                                                                                                                                                                                                                                                                                                1. .964
/organism="Solanum tuberosum"
/mol type="mRNA"
/cultivar="Kennebec"
/db xref="taxon:4113"
/clone="POABE14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Solanum tuberosum (potato)
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and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d. Set 4 were grown under the standard conditions and then were heat stressed by placement at 35 C. Heat stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, and 4d. RNA was isolated from all tissues and equal RNA from each tissue and stress was pooled to construct the cDNA library. RNA sample."

356 340 376 396 416 160 297 ArgfyrArgGlnTyrHisHisGlnMetGlnIleIleValLeuSerPheGluGlnValAla 316 220 336 280 400 460 520 436 580 456 640 GluMetTyrLeuGluGluVallys-----AsnGlnGluGlnAsnSerThrAsnThrSer 474 700 276 277 ArgGlnGluLeuGlnMetLysLysAlaLysLeuLeuAlaMetLeuGluGluValGluGln 296 GlyAspAsnLysAsnLysGluThrAsnIleSerAlaProAsnGluGluLysHisProIle 494 237 AsnSerMetAsnLysGluSerMetProLeuAlaSerAspValAsnThrAsnSerSerGly 256 ---GATGTTGAAAGTAGCAGCCAAAAAAT---ATTGTTGTTGTTGAACTTACTACAGCTCAA ArgCysLeuLysAspAlaIleAlaGluGlnValLysAlaThrSerLysSerLeuGlyGlu ArgGlnGlnArgAlaLeuGlnGlnIleGlyMetMetGlnProAsnAlaTrpArgProGln GAAATGTACATGGAAGAAGTGAAGAAACCAATCAAGAACAAAATTTGAGCCTAATAAC IleThrSerSerLeuLeuGlnAspGlyIleThrThrThrGlnAlaGluIleSerThrSer GlyIleGlySerAlaLysSerTyrThrGlnLeuAlaLeuHisAlaIleSerLysGlnPhe HisProTyrProLysAspSerAspLysIleMetLeuAlaLysGlnThrGlyLeuThrArg SerGlnValSerAsnTrpPheIleAsnAlaArgValArgLeuTrpLysProMetValGlu AGCCAGGTATCAAATTGGTTTATAAATGCTAGAGTTAGACTATGGAAGGCCAATGGTAGAA 257 GlyGlyGluSerSerSerArgGlnLysAsnGluValAlaValGluLeuThrThrAlaGln CACAAATTGGACAATGAATTAATATCTTTGGCTAGTGAT-------964 226 37 51 27 Length:
Matches:
Conservative:
Mismatches:
Indels: US-10-624-201A-2 (1-688) x CK262102 (1-964) 6.08e-98 1057.00 77.35% 66.47% 29.67%

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ORGANISM ACCESSION VERSION KEYWORDS SOURCE

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FEATURES

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BG129304 630 bp mRNA linear EST 31-JAN-2001 EST474950 tomato shoot/meristem Lycopersicon esculentum cDNA clone cTOF23112 5' sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lycopersicon esculentum (tomato)
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 630)
van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Utterback,T.,
Hansen,C., Ronning,C. and Tanksley,S.
Generation of ESTs from tomato shoot/meristem tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          522 AlaGlyAlaSerLeuHisHisAlaHisAsnPheSerPheLeuGlySerPheAsnMetAsp 541
                                                                                                                                                                                                                                                                462 GluValLysAsnGlnGluGlnAsnSerThrAsnThrSerGlyAspAsnLysAsnLysGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuGlnGlnIleGlyMetMetGlnProAsnAlaTrpArgProGlnArgGlyLeuProGlu
                                                                                                  ArgalavalSerValLeuArgalaTrpLeuPheGluHisPheLeuHisProTyrProLys
                                                                                                                            123 AGAGCTGTCTCTGTCCTTCGTGCTTGGCTTTTTCGAGCATTTTCTTCATCCTTACCCCAAA
                                                                                                                                                                                   422 AspSerAspLysIleMetLeuAlaLysGlnThrGlyLeuThrArgSerGlnValSerAsn
                                                                                                                                                                                                             183 GACTCAGACAAAATCATGCTTGCTAAGCAAACGGGGCTAACAAGGAGCCAGGTCTCTAAC
                                                                                                                                                                                                                                                                                                                                                                                              303 GAAGTGAAGAATCAAGAACAAAACAGTAGTAATACTTCAGGAGATAACAAAAAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    502 AspGlyIleThrThrThrGlnAlaGluIleSerThrSerThrIleSerThrSerProThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          537 AATACTACTACTACTGTTGATCATATTGAAAACAACGCGAAAAAAGCCAAAAAAGCAAAAAACAAGAAAATCATGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  561 MetHisLysPheSerProSerSerIleLeuSerSerValAspMetGlu 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="shoot/meristem"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:4081"
/clone="cTOF23N12"
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EST340678 tomato fruit mature green, TAMU Lycopersicon esculentum
CDNA clone cLEF41L1 5', mRNA sequence.
AW930221
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By Marayota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.

(bases 1 to 644)

Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F.,

Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S.,

Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
859
                                                                                                                                                                    860 TTCTCCTTCATTAGGTCATTAAACATGGAGAAC-----ATTGATGATGATCAAAGG 907
                                                                                                                                                                                                                          362 GlyLysIleGluGlySerArgLeuLysPheValAspHisHisLeuArgGlnGlnArgAla 381
                                                              531
                                                                                                                                           PheserPheLeuGlySerPheAsnMetAspAsnThrThrThrValAspHisIleGlu 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="tomato fruit mature green, TAMU"
/note="Vector: pBlueScript SK(-); Site 1: EcoR1; Site_2:
Xhol; cLEF - Fruit were tagged at the Icm stage and
harvested 3-5 days prior to ripening. Fruit were cut in
half to verify the seeds were indeed 'immature' and the
seeds and locules were discarded prior to freezing the
pericarp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ThrIleSerThrSerProThrAlaGlyAlaSerLeuHisHisAlaHis------Asn
                                                                                                    800 ACCATTTCAACATCTCCGACAGGGGGGGGGTTCGATTCCGGCTCAGACGGTTGCAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .644

/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cullivar="TA496"
/db_xref="taxon:4081"
/clone="chEF4111"
/tissue_type="fruit pericarp"
/dev_stage="mautre green (3-5 days pre-ripening)"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
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603
44
23
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Generation of ESTs from tomato fruit tissue
Unpublished (1999)
Contact: CUGI
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Matches:
Conservative:
Mismatches:
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1043.50
96.76%
93.98%
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Pred. No.:

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Sequence

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/mol type="mmk"
/mol type="mmk"
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/cultivar="Nokkwang"
/db xref="taxon:4012"
/tissue type="red pepper fruit pericarp"
/tissue type="red pepper fruit pericarp"
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/note="Vector: pBluescript II SK(+)XR; Site_1: EcoRI;
/int_ pericarp using lambda Zap II phage vector. In vivo excision was done with helper phage to generate subclone in pBluescript II SK(+)XR) vector."
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   l (bases 1 to 610)
Song, W.Y., Jeon, W.B., Kim, K.S., Lee, H.H., Ko, M.K., Kim, Y..
Hong, J.C. and Ohl B.J.
Generation of Hot Paper (Capsicum annuum) ESTs (Express Tags) from Red Ripe Fruit (Song, et al.)
                                                                                                                                                                                                                                                                                                                                                                                       610
192
5
3
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                     Contact: Boung-Jun Oh
Jeonnam Biotechnology Research Center
Namyang Bld. #603, 10-4 Gwangsan-dong,
                                                                                                                                                                                                    1. .610
/organism="Capsicum annuum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                    Tel: 82 62 607 2422
Fax: 82 62 607 6205
Email: bjo@biohub.re.kr
Plate: 039 row: F column: 01.
Location/Qualifiers
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981.50
95.63%
93.20%
27.55%
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Percent Similarity:
Best Local Similarity:
Query Match:
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Pred. No.:
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CDNA 5', mRNA sequence.
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/lab_host="SOLR"
/clone_lib="tomato shoot/meristem"
/note="Vector: pBluescript SK(-); Site_1: EccR1; Site_2: Ahol; Small expanding leaves from the growing tip were taken from greenhouse plants (4-6wks old TA496). Tissue was immediately frozen in liquid nitrogen."
                                                                                                                                                                                                                                                                      GluasnasnalalyslysGlnargasn---AspmethislyspheserproserSerile
                                                                                                                                                                                                                                      3 TGGAAGCCAATGGTTGAAGAAATGTACTTGGAAGAAGAGAGAATCAAGAATCAAAAACAGT
                                                                                                                                                                                                                                                                                                                                      LeuSerServalaspMetGluAlaLysAlaArgGluSerSerAsnLysGlyPheThrAsn
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                                                                                                                                                                                                                       TrpLysPrometValGluGluMetTyrLeuGluGluValLysAsnGlnGluGlnAsnSer
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196
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                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
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BJ02039F01 BJ02 Capsicum annuum
CO909070 GI:51299373
EST.
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                                                                                                          1.03e-92
1003.50
95.73%
92.89%
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Best Local Similarity:
Query Match:
DB:
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Oryza sativa (indica cultivar-group)

ISM Oryza sativa (indica cultivar-group)

ENKarycota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

Enrhartoideae; Oryzeae; Oryza.

I (bases 1 to 1965)

RS Ma, L., Wangc, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M., Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L., Mong, G. K.S., Deng, X., and Wang, J.

An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis

An unpublished (2004)

Contact: Chen Chen

Department of Bioinformatic

Baijing Institute of Genomics

Chinese Academy of Sciences, Beijing 101300, China

Tel: 86-10-80488676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1965 bp DNA linear GSS 21-SEP-2004 OGIFCC012180 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence. CL978605 GSS-1 GI:52411712 GSS.
                                                                                                                                                                                                        447
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                                                                                                                                                                                                                                                                       448 CATGGACTTTTACAGCGCATGTGGAACAACCAAGATCAATCTCAGCAGGTGATACTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                  SerSerProAlaAlaSerAsnAlaLeuCysHisAlaAsnIleGlnHisAlaProLeuGln
                                                                                                                                                                                           /clone lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences
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Rice genomic sequence.
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Pred. No.:
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COMMENT
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E 1 (base 1 to 69.9)

S Buell, C.R., Hart, A., Baker, B., Tanksley, S., Fry, W., Smart, C., Restrepo, S., Griffiths, H., van der Hoeven, R., Tsai, J. and Karamycheva, S.A.
Generation of a set of potato cDNA clones for microarray analyses Unpublished (2002)

On Apr 17, 2002 this sequence version replaced gi:20171732.
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850, USA
                                                                                                                                                                                                                              BQ119770 699 bp mRNA linear EST 07-MAR-2003 EST605346 mixed potato tissues Solanum tuberosum cDNA clone STMEMS4 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue type="mixed tissues"
/lab_host="SOLR"
/lab_host="SOLR"
/clone lib="mixed potato tissues"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; supplier: Combination of untreated and Phytophthora
infertans -treated libraries of stolons, leaves, leaflets,
axillary buds of stem explants, petioles, germinating
eyes, tubers, or roots."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LysGlnThrGlyLeuThrArgSerGlnValSerAsnTrpPheIleAsnAlaArgValArg 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148 ATGTACTATCAAGGAACCTCGGATAATACTAATATACAAGCTGATCATCAACAACATCAT
                                                                           MetTyrTyrGlnGlyThrSerAspAsnThrAsnIleGlnAlaAspHisGlnGlnArgHis
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Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"

cultivar="kennebec or Binjte"

db_xref="taxon:4113"

clone="STMEM54"
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                                                                                                                                    450 LeuTrpLysProMetVal 455
                                                                                                                                                                     592 crarccaaccaarccic 609
                                                                                                                                                                                                                                                                                                                       BQ119770.2 GI:21919664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /done liber potato microtubers, in vitro-grown"
//done liber potato
//done liber potato
//done liber potato
//done liber potato SK(-); Site l: EcoRI; Site_2:
Xhol; Tissue supplied by Christian Bachem and Richard
Visser (Department of Plant Breeding, Wageningen
University, The Netherlands); sequencing by The Institute
for Genomic Research. The cSTA libraries will attempt to
capture the induction and initiation/initial growth of the
tuber in an in vitro system as described in Bachem et al.
(Plant Journal, 1996). Small microtubers develop from
axillary buds attached to stem explants when placed on a
high sucrose medium (10%). Visible morphological changes
occur synchronously at day five in the axillary buds.
first library, cSTA (1-20) consists of axillary buds
harvested on days 1-3. This targets those genes involved
in induction of the microtubers. The following libraries,
cSTA (21-40) and cSTA (41-60), capture genes involved in
tuber initiation and outgrowth. This library is noted as
P3 in Tanksley lab notebooks."
                                                                                                                                                                                                                                                                                                                 708 bp mRNA linear EST 10-MAR-2003
EST540875 potato microtubers, in vitro-grown Solanum tuberosum cDNA
E1920940
1750 TTCGCGTTCGCCGGGCACGCCGCGGAGGCGGCGGCGCGCGTGTCGCTCACGCTCGGCCTC 1809
                                                                                                                                                     Solanum tuberosum

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

1 (bases 1 to 708)

van der Hoeven,R., Bezzerides,J., Bachem,C., Visser,R.,

Karamycheva,S.A., Tsai,J., Van Aken,S., Utterback,T., Chiemingo,A.,

Bougri,O., Buell,C.R., Ronning,C., Tanksley,S. and Baker,B.

Generation of ESTs from in vitro grown microtubers (2001b)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The Institute for Genomic Research 9712 Medical Center Dr. Rockville, MD 20850, USA Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
                                                                                                                          647 GlySerArgSerGluMetGlySerHisTyrAsnArgMetGlyTyrGluAsnIleAspPhe 666
                                                                 627 ProProSerGluAsnLeuAlaMetProValSerGlnGlnAsnTyrLeuSerAsnAspLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         stem explants; growing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue type="axillary buds of sink-tubers"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="7, 8 and 10 days"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .708
/organism="Solanum tuberosum"
/mol type="mRNA"
/culTivar="Bintje"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         db_xref="taxon:4113"
/clone="cSTE26N18"
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                                                                                                                                                                                                                                                                                                                                                                                                                                       BI920940.1 GI:16216968
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AUTHORS
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COMMENT
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FEATURES

Alignment Scores:

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Lycopersicon esculentum
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 623)
Alcala,J., Verbalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F.,
Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S.,
Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW441343 tomato fruit red ripe, TAMU Lycopersicon esculentum cDNA clone cLEN15B11 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        287 AATICTICACCAGCAGGAAGCAACGCGCTTTGCCATGCGAATATACAACACGCGCCGCTG 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     407 CAICAIGGACTITIACAGCGTAIGTGGAACAACCAAGAICAAICTCAGCAGGIGAIAGIA 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            527 CAATTGGCGTTTCAGAGGCCGATTGTGGTGTCGGAACACCGACAGCAGCAACAACAGCAA 586
                                                                                                                                                                                                                                                                             110 ATGTACTATCAAGGAACCTCGGATAAT---AATATACAAGCTGATCATCAACAACATCAT 166
                                                                                                                                                                                                                                                                                                                                                                                                                                   59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 IleSerSerSerProArgThrAsnAsnValThrIleArgGlyThrLeuAspGly 198
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647 ATTICAGCCTCATCACCAAGACAATAATGTTACTATTAGAGGAAGATTAGATGGG 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 347 CAACAGCAGCTTTGTCGGTGTGCCTCTTCCGGCAGTAAGTTTGCACGATCAGATCAAT
                                                                                                                                                                                                                              MetTyrTyrGlnGlyThrSerAspAsnThrAsnIleGlnAlaAspHisGlnGlnArgHis
                                                                                                                                                                                                                                                                                                                               AsnHisGlyAsnSerAsnAsnAsnAsnIleGlnThrLeuTyrLeuMetAsnProAsnAsn
                                                                                                                                                                                                                                                                                                                                                                                                                              100 HisHisGlyLeuLeuGlnArgMetTrpAsnAsnGlnAspGlnSerGlnGlnVallleVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         467 CCATCGTCGACGGGGGTTTCTGCCACGTCATGTGGCGGGGTTACCACGGACTTGGCGTCT
708
186
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Generation of ESTs from tomato fruit tissue
Unpublished (1999)
Length:
Matches:
Conservative:
Mismatches:
Indels:
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Clemeon University Genomics Institute
Clemeon University
100 Jordan Hall, Clemson, SC 29634, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lycopersicon esculentum (tomato)
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3.01e-88
961.00
94.97%
93.47%
26.97%
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/organism="Lycopersicon esculentum"
/mol type="mRNA"
/mol type="mRNA"
/mol type="mRN1-12 (35S::Pto in Rio Grande x Money Maker)"
/db xref="taxon:4081"
/clone="cLRR5L8"
/dissue type="leaf"
/dv stage="4-week old"
/lab host="80lx"
/clone lib="tomato resistant, Cornell"
/clone lib="tomato resistant, RK(-); Site 1: EcoR1; Site 2:
/note="Vector: pBlueScript SK(-); Site 1: EcoR1; Site 2: EcoR1; Site 3: 
                                                                                                                                                     EST 18-MAY-2001
                                                                                                                                                                                                                                                                                                                 Lycoperation esculentum
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
1 (bases 1 to 55)
1 Liang, F., Upton, J., Roming, C.M., Craven, M.B., Fujii, C.Y.,
Bowman, C.L., Nierman, W., Praser, C.M., Venter, J.C., Tanksley, S.D.,
Giovannoni, J.J. and Martin, G.B.
Generation of ESTs from Pseudomonas resistant tomato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ArgGlnGlnArgAlaLeuGlnGlnIleGlyMetMetGlnProAsnAlaTrpArgProGln 396
                                                                                                                                A1773253
EST224353 tomato resistant, Cornell Lycopersicon esculentum cDNA
COLOGE CLERSLB, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     317 GlylleGlySerAlaLysSerTyrThrGlnLeuAlaLeuHisAlaIleSerLygGlnPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ArgCysLeuLysAspAlaIleAlaGluGlnValLysAlaThrSerLysSerLeuGlyGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: CUGI
Clemson University
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
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                                                                                                RESULT 11
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                                                                                                                                                          /db_xref="taxon.40s"
/db_xref="taxon.40s"
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/tissue_type="pericarp"
/dev_stage="tred rice (7-20 days post-breaker)"
/dev_stage="tred rice (7-20 days post-breaker)"
/clone lib="tomato fruit red rice, TAMU"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xho1; supplier: Glovannoni; Fruit were tagged at the
breaker stage (first sign of lycopene accumulation on the
blossom end of the fruit) and harvested 7 days
post-breaker (fully red-ripe), 10 days post breaker, and
20 days post-breaker (over-ripe), 20 day fruit which
showed external or internal signs of pathogenesis were
discarded. Fruit were cut in half and the seeds and
locules were discarded prior to freezing the pericarp."
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Bmail: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
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                                                                                             /organism="Lycopersicon esculentum"
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cultivar="TA496"
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ligated into the pBluescript pBluescript II XR cDNA Libra to manufacturer's instructio (Stratagene). Plasmid DNA wa electroporation into DH10B c propagation. Normalization w published methods [Bonaldo M Research 6 (9):791] in order' highly expressed transcripts	: 1.22e-81 898.00 by: 73.72% arity: 62.80% 25.20%	US-10-624-201A-2 (1-688) x CV241175 (1-827) Qy 155 GlnGlnGlnGlnGlnGlyGlyLeuSerLeuSerLe B20 CAGGCTCAAACTGTATCTGGTGAAGATATAAGGGT Qy 175 SerPheAsnAsnAsnIleSerSerSerProAr	195 ThrLe 736 215 Glule 688 GAGCT	2 8 3 8 5 6 2 8 6 8 6 8 8 6 8 8 8 8 8 8 8 8 8 8 8	273 520 293 460 313	Oy 313 SeriysGlnPheArgCysleulysAspAlaileAl
Qy 397 ArgGlyLeuProGluhxgAlaValSerValLeuArgAlaTrpLeuPheGluHisPheLeu 416 Db 243 AgAGGTTTACCTGAAGAGCTGCTCTGTGCTTGGCTTTTCGAGCATTTTCTT 302 Qy 417 HisProTyrProLysAspSerAspLysIleMetLeuAlaLysGlnThrGlyLeuThrArg 436 Db 303 CATCCTTACCCCAAGAGCTCAGACAAATCTGCTAAGCAAAGCGGCTAACAAGG 362 Qy 437 SerGlnValSerAsnTrpPheileAsnAlaArgValArgLeuTrpLysProMetValGlu 456 Db 363 AGCCAGCTCTCTAATTAATGCTCCAATTAATGCTATAAAGGCTAAAAGCTAAAAAGCTCAATTAATAGGTTCAATTAATAGGTTCAATTAAAAGCTCCAATTAAAAAGCTCAATTAATAGGTTCAATTAAAAGGTTCAATTAATAGGTTCAATTAAAAAGCTCAATTAAATAGGATTCAATTAAAAAGCTCAATTAAATAGGATTCAATTAAAAAAAA	457 GluMetTyrLeuGluGluValLysAsnGlnGluGlnAsnSerThrAsnThrSerGlyAsp 47	Oy 497 SerSerLeu 499		rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus. 1 (bases I to 827). AUTHORS Ralph, S., Cooper, D., Kolosova, N., Oddy, C., Butterfield, Y., Kirkpatrick, R., Liu, J., Palmquist, D., Stott, J., Barber, S., Yang, G., Babakaiff, R., Brown-John, M., Chand, S., Featherstone, R., Masson, A., Mayo, M., Moran, J., Olson, T., Wong, D., Ritland, C.E., Siddiqui, A., Holt, R., Jones, S., Marra, M., Ellis, B.E., Douglas, C., Ritland, K. and Bohlmann, J. TITLE The poplar transcriptome: Analysis of expressed sequence tags from	multiple cDNA libraries JOURNAL Unpublished (2004) CONTACT: Joerg Bohlmann Genome BC forest genomics program University of British Columbia University of British Columbia University Baltish Columbia Vancouver, British Columbia, 6174 University Boulevard, Rm. 237, Vancouver, British Columbia, Canada, V6T 123 Tel: 1-604-822-0697 Eax: 1-604-822-6097 Enail: bohlmann@interchange.ubc.ca Plate: W905531 row: G column: 23 High quality sequence stop: 877.	FEATURES Location/Qualifiers 1. 827 1. 827 1. 827 1. 827 1. 827 1. 827 1. 827 1. 827 1. 827 1. 827 1. 827 1. 827 1. 827 1. 827 1. 827 1. 827 1. 827 1. 828

ript II SK (+) XR vector using the library Construction Kit according ctions with modifications

(A was then transformed by OB cells (Invitrogen) for on was applied according to do M.F. et al. (1996) Genome der to reduce the abundance of ipts."

Lysalalysleuleualametleuglu 292 ArgThrAsnAsnValThrIleArgGly 194 GlySerLysTyrLeuLysAlahlaGln 214 ||||||| |ATGATATTAAGAGTGAATTGTCAAAG 629 MetProLeuAlaSerAspValAsnThr 252 AAAGTGGTTGGAGAATCATTAGCCGGA 569 31nLysAsnGluValAlaValGluLeu 272 GT------GGACCGGAGCTT 521 ysserijelysglyaspaspglnlys 234 euserProglnLeuGlnGlnGlnIle 174 827 184 32 32 22 4 tive: e8:

SlnIleGlyMetMetGlnProAsnAla 392 ValSerValLeuArgAlaTrpLeuPhe 412 TyrThrGlnLeuAlaLeuHisAlaile 332 ||||||| |TATACAGCCCTTGCGCTGAAACAATC 341

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/done liber source
/note="Wector: pBluescript SK(-); Site 1: EcoRI; Site_2:
Xhoi; Tissue supplied by Christian Bachem and Richard
Visser (Department of Plant Breeding, Wageningen
University, The Netherlands); sequencing by The Institute
for Genomic Research. The cSTA libraries will attempt to
capture the induction and initiation/initial growth of the
tuber in an in vitro system as described in Bachem et al.
(Plant Journal, 1996): Small microtubers develop from
axillary buds attached to stem explants when placed on a
high sucross medium (10%). Visible morphological changes
occur synchronously at day five in the axillary buds
first library, cSTA (1-20) consists of axillary buds
harvested on days 1-3: This targets those genes involved
in induction of the microtubers. The following libraries,
cSTA (21-40) and cSTA (41-60), capture genes involved in
tuber intiation and outgrowth. This library is noted as
P3 in Tanksley lab notebooks."
                                                                                                                                                                                                                                                                                                 Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; laminds; Solanales; Solanaceae; Solanum.
1 (bases 1 to 789)
van der Hoeven,R., Bezzerides,J., Bachem,C., Visser,R.,
Karamycheva,S.A., Tsai,J., Van Aken,S., Utterback,T., Chiemingo,A.,
Bougri,O., Buell,C.R., Ronning,C., Tanksley,S. and Baker,B.
Generation of ESTS from in vitro grown microtubers (2001b)
                                                                                                                                                                             B1921008
789 bp mRNA linear EST 10-MAR-2003 EST540943 potato microtubers, in vitro-grown Solanum tuberosum cDNA clone cSTE27121 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
   432
/tissue type="axillary buds of stem explants; growing sink-tubers"
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Mismatches:
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Gaps:
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Department of Botany & Plant Sciences, University of California
Riverside, CA, 92521-0124
Tel: 9097871318
Fax: 9097874437
Email: timothy.close@ucr.edu
Seq primer: T7
                                                                                                                                                                    342 AATCATGGGAATAGTAATAATAATAATATTCAGACACTTTATTTGATGAACCCTAACAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           522 CAGCAGCACTTTGTCGGTGTGCCTCTTCCGGCAGTAAGTTTGCACGATCAGTCAATCAT
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                                                                                                                                             TyrMetGlnGlyTyrThrThrSerAspThrGlnGlnGlnGlnGlnLeuLeuPheLeuAsn
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheog
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheog
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Sapindales; Rutaceae; Citrus.
1 (bases I to 850)
Close,T.J., Collura,K., Fenton,R.D., Feuerbacher,O., Kim,H.R
Rudrna,D., Wanamaker,S., Wing,R. and Yu,Y.
Development of EST Resources and New Genetic Markers for Cal:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol type="mRNA"
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CB292855
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556 469

451

431

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752 bp mRNA linear EST 20-FEB-2002
ESTS86759 tomato breaker fruit Lycopersicon esculentum cDNA clone
CLEG67P6 5' end, mRNA sequence.
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Alcala,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A., Tsai,J., Bougri,O., Kirkness,E., Utterback,T., Van Aken,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
                                                                                                                                                                                                                               437 TTCGAACACTTCCTTCACCCGTATCCGAAGATTCGGACAAGCAGATGCTGGCAAAACAA 496
                                                                                                                                                                                                                                                                                                                                                                                            476 AspAsnLysAsn----LysGluThrAsnIleSerAlaProAsnGluGluLysHisPro 493
                                                                                                                                                                                                                                                                                                                                                                                                                                             677 CAAGAGAAAATCTCGTGAAGGAAACTCAAAACTCGAAGAGTTTCAAATCCAGTGAGGAT 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194 IlelleThrSerSerLeuLeuGlnAspGlyIleThrThrThrGlnAlaGluIleSerThr 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    737 AATTTGACAAACCAG---------AATGTTCATTCTATGATTTCAATG 775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  514 SerThrileSerThrSerProThrAlaGlyAlaSerLeuHisHisAlaHisAsnPheSer 533
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Generation of ESTs from tomato fruit tissue, breaker stage (2002)
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
Institute
                   PheGluHisPheLeuHisProTyrProLysAspSerAspLysIleMetLeuAlaLysGln
                                                                                                             ThrGlyLeuThrArgSerGlnValSerAsnTrpPheIleAsnAlaArgValArgLeuTrp
                                                                                                                                                           497 ACAGGGCTTACCAGGAGCCAGGTGTCTAATTGGTTCATAAATGCACGAGTTCGGCTGG
                                                                                                                                                                                                         LysProMetValGluGluMetTyrLeuGluGluValLysAsnGlnGluGlnAsn-----
                                                                                                                                                                                                                                                                                                   ------SerThrAsnThrSerGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Lycopersicon esculentum"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="clbg67P6"
/tissue_type="Pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
/clone_lib="tomato breake
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lycopersicon esculentum (tomato)
Lycopersicon esculentum
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/cultivar="TA496"
/db_xref="taxon:4081"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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ORGANISM
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            /dev stage="Mature Fruit"
//lab hose="E. coli TUC121"
//clone_lib="Washington Navel orange cold acclimated
//clone_lib="Washington Navel orange cold acclimated
flavedo & albedo CDNA library"
//note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: Ecoli Site_2: XhOI; Plants were grown in the
field at University of California, Riverside Agricultural
Operations since 1983. The scion was Washington Navel
orange and the rootstock Carizoc Citrange. Tissue from
mature fruit was harvested at mid-day in January 2002
during a cold spell, when pre-dawn temperatures were
approximately -2 to 2 degree C. Approximately 2 cm median
sections of the rind were excised in the field from
several fruits, then wrapped in aluminum foll and frozen
quickly in dry ice. Total RNA was extracted using a phenol
extraction procedure described in J. Japanese Soc. Hort.
Sci. (1996) 64:809-814. Poly(A) RNA was purified, a cDNA
library was made, and 1 million primary lambda cDNA
library was made, and 1 million primary lambda cDNA
library was made, and 1 million primary lambda cDNA
library was made, and 1 million primary lambda cDNA
library was made, and 1 million primary lambda cDNA
library was made, and 1 million primary lambda
kiverside (Fenton). Phagemids were plated, plasmid DNA
purified, cDNA clones archived, and DNA sequences
determined bi-directionally using an AB1530 at the
Arizona Genomics Institute, University of Arizona
(Collura, Feuerbacher, Kim, Kudrna, Wing, Yu).
Chromatogram files were transmitted to UC Riverside (by Wanamaker) using
the HarvEST pipeline (http://harvest.ucr.edu) to remove
vector and cloning oligo sequences and various
contaminants, and to trim to a high quality region.
Sequences that retained a phred 17 region of at least 100
bases were deposited to GenBank."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATGAGGTGGAGCAAAGGTACCCGTTGAACCATCACCAGATGCAGATAGTGATTTCATCA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluGluValGluGlnArgTyrArgGlnTyrHisHisGlnMetGlnIleIleValLeuSer 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTGAACAAGCAGCAGCAATTGAGTCAGCAAAGACATACACAGCACTTGCTCTCAAGACA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IleSerLysGlnPheArgCysLeuLysAspAlaIleAlaGluGlnValLysAlaThrSer 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LysSerLeuGlyGluGluGlyLeuGlyGlyLysIleGluGlySerArgLeuLysPhe 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTCGACCACCATCTTCGTCAACAAAAGGGTCTTCAACAATTGGGAATGATCCAGCACAAAT 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCTTGGAGACCCCCAAAGAGGATTGCCTGAAAGATCTGTCTCAGTTCTTCGCGCTTGGCTC 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PheGluGlnValalaGlyIleGlySerAlaLysSerTyrThrGlnLeuAlaLeuHisAla 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuThrThrAlaGlnArgGlnGluLeuGlnMetLysLysAlaLysLeuLeuAlaMetLeu 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tissue type="Rind containing flavedo and albedo'
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Mismatches:
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Site_2: XhoI; supplier: Boyce Thompson Institute, sequencing: The Institute for Genomic Research. Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."
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ArgGlnGluLeuGlnMetLysLysLysLysLeluLeuAlaMetLeuGluGluValGluGln 296 GlylleGlySerAlaLysSerTyrThrGlnLeuAlaLeuHisAlalleSerLysGlnPhe 336 416 519 rgSerGlnValSerAsnTrpPheIleAsnAlaArgValArgLeuTrpLysProMetValG 456 276 356 339 396 459 436 579 luGluMetTyrLeuGluGluValLys-----AsnGlnGluGlnAsnSerThrAsnThrS 474 691 237 AsnSerMetAsnLysGluSerMetProLeuAlaSerAspValAsnThrAsnSerSerGly 256 45 99 257 GlyGlyGluSerSerSerArgGlnLysAsnGluValAlaValGluLeuThrThrAlaGln ---GATATTGAAAGTAACACCCAAAAAAATAGT---GGTGTTGAACTTACAACAGCTCAA 752 188 19 27 18 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: erGlyAspAsnLysAsnLysGluThrAsn 483 ----GATCAAAAATTATTGAACCTAAT (1-752)US-10-624-201A-2 (1-688) x BM535737 7.91e-81 889.50 82.47% 74.90% Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores: Pred. No.: 100 220 (280 396 520 460 580 456 640 277 317 46 337 416 436 474 8 원 8 8 6 6 6 6 6 8 & 8 8686 જે 셤 ઠે a දු දු g ें

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